

OM protein - protein search, using sw model

Run on: September 15, 2004, 08:32:22 ; Search time 125 Seconds  
 (without alignments)  
 716.540 Million cell updates/sec

Title: US-09-211-315-39  
 Perfect score: 1685  
 Sequence: 1 MRRASRDYTKYLRGSEEMGG.....LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
 1: geneseqp1980s:\*  
 2: geneseqp1990s:\*  
 3: geneseqp2000s:\*  
 4: geneseqp2001s:\*  
 5: geneseqp2002s:\*  
 6: geneseqp2003as:\*  
 7: geneseqp2003bs:\*  
 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1685	100.0	317	2	AAW83195	Aaw83195 Human ost
2	1685	100.0	317	2	AAW69957	Aaw69957 NF-kB rec
3	1685	100.0	317	2	AAW68293	Aaw68293 NF-kB rec
4	1685	100.0	317	2	AAE08738	Aae08738 Human rec
5	1685	100.0	317	3	AAY84417	Aay84417 Amino aci
6	1685	100.0	317	4	AAE04426	Aae04426 Human rec
7	1685	100.0	317	4	AAE01993	Aae01993 Human ful
8	1685	100.0	317	5	ABB08134	Abb08134 Human RAN
9	1685	100.0	317	5	AAE26103	Aae26103 Human RAN

10	1685	100.0	317	5	ABG31631	Abg31631	Human	RAN
11	1685	100.0	317	5	AAU78285	Aau78285	Human	TRA
12	1685	100.0	317	5	AAO19096	Aao19096	C neoform	
13	1685	100.0	317	6	ABP55108	Abp55108	Human	ost
14	1685	100.0	317	6	AAE34364	Aae34364	Human	rec
15	1685	100.0	317	6	ABR42314	Abr42314	Human	RAN
16	1685	100.0	317	7	ADB16988	Adb16988	Human	rec
17	1685	100.0	317	7	ADC35204	Adc35204	Human	TNF
18	1685	100.0	317	7	ADC73002	Adc73002	Human	RAN
19	1685	100.0	317	7	ADC78268	Adc78268	Human	RAN
20	1677	99.5	317	2	AAW83018	Aaw83018	Osteoclas	
21	1417.5	84.1	316	2	AAW83017	Aaw83017	Osteoclas	
22	1417.5	84.1	316	2	AAW83194	Aaw83194	Human	ost
23	1417.5	84.1	316	2	AAW59654	Aaw59654	Amino	aci
24	1417.5	84.1	316	2	AAyl7874	Aayl7874	Murine	TR
25	1417.5	84.1	316	3	AAy91024	Aay91024	Mouse	OBM
26	1417.5	84.1	316	3	AAy84418	Aay84418	Amino	aci
27	1417.5	84.1	316	3	AAy84419	Aay84419	Amino	aci
28	1417.5	84.1	316	5	AAU78289	Aau78289	Mouse	TRA
29	1417.5	84.1	316	6	ABR42071	Abr42071	Human	RAN
30	1417.5	84.1	316	6	ABB99477	Abb99477	Amino	aci
31	1417.5	84.1	316	6	ABU08463	Abu08463	Amino	aci
32	1417.5	84.1	316	6	ABR55560	Abr55560	Amino	aci
33	1396.5	82.9	318	4	AAB82092	Aab82092	Rat	osteo
34	1326.5	78.7	294	2	AAW69956	Aaw69956	NF-kB	rec
35	1326.5	78.7	294	2	AAW68292	Aaw68292	NF-kB	rec
36	1326.5	78.7	294	2	AAE08737	Aae08737	Murine	re
37	1326.5	78.7	294	4	AAE04425	Aae04425	Murine	re
38	1326.5	78.7	294	4	AAE01992	Aae01992	Murine	RA
39	1326.5	78.7	294	5	AAE26102	Aae26102	Mouse	RAN
40	1326.5	78.7	294	7	ADB16986	Adb16986	Murine	re
41	1326.5	78.7	294	7	ADC73000	Adc73000	Murine	RA
42	1326.5	78.7	294	7	ADC78266	Adc78266	Murine	RA
43	1325	78.6	250	6	ADA50079	Ada50079	Human	wil
44	1322	78.5	250	6	ADA50095	Ada50095	Human	RAN
45	1322	78.5	250	6	ADA50094	Ada50094	Human	RAN

# ALIGNMENTS

## RESULT 1

AAW83195

ID AAW83195 standard; protein; 317 AA.

XX

AC AAW83195;

XX

DT 11-FEB-1999 (first entry)

XX

DE Human osteoprotegerin binding protein from the pcDNA/huOPGbp1.insert.

XX

KW Human; osteoprotegerin binding protein; OPG binding protein; arthritis;

KW osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;

KW hypercalcaemia; osteoclast differentiation and activation receptor;

KW Paget's disease.

XX

OS Homo sapiens.

XX  
PN WO9846751-A1.

XX  
PD 22-OCT-1998.

XX  
PF 15-APR-1998; 98WO-US007584.

XX  
PR 16-APR-1997; 97US-00842842.

PR 23-JUN-1997; 97US-00880855.  
PR 30-MAR-1998; 98US-00052521.

XX  
PA (AMGE-) AMGEN INC.

XX  
PI Boyle WJ;

XX  
DR WPI; 1998-594578/50.

DR N-PSDB; AAV70285.  
XX

PT Nucleic acid encoding osteoprotegrin binding protein - useful for, e.g.  
PT treating bone diseases by modulating osteoclast differentiation and for  
PT diagnosis.

XX  
PS Claim 19; Fig 4; 47pp; English.

XX  
CC The present sequence is human osteoprotegerin (OPG) binding protein. Host  
CC cells transfected with vectors containing nucleic acid molecules encoding  
CC OPG binding protein are used to produce recombinant OPG binding protein.  
CC OPG binding protein is used in binding assays to determine osteoprotegrin  
CC (OG) in biological samples; to screen for specific binding agents  
CC (particularly agonists and antagonists, including intracellular proteins)  
CC ; to raise Ab (useful in immunoassays for detection of OPG binding  
CC protein) and to identify compounds that modulate binding of OPG binding  
CC protein to osteoclast differentiation and activation receptor (ODAR). The  
CC nucleic acid molecule encoding OPG binding protein can be used to detect  
CC OPG binding protein-encoding sequences, e.g. screening for related  
CC sequences, also to produce transgenic animal models, while complementary  
CC sequences are used for antisense regulation of OPG binding protein  
CC expression. Modulators of OPG binding protein, particularly soluble forms  
CC of OPG binding protein or Ab, are used to treat or prevent bone diseases,  
CC e.g. osteoporosis, bone loss caused by arthritis or metastases,  
CC hypercalcaemia, Paget's disease, periodontal disease, osteoporosis,  
CC loosening of prostheses, optionally in combination with agents that  
CC promote bone growth

XX  
SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 2; Length 317;

Best Local Similarity 100.0%; Pred. No. 4.3e-154;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY            1 MRRASRDYTKYLRGSEEMGGGPAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLQQV   60  
| | | | |

Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

[illegible]

Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH	180
Db	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH	180
Qy	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV	240
Db	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV	240
Qy	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD	300
Db	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD	300
Qy	301	PDQDATYFGAFKVRDID	317
Db	301	PDQDATYFGAFKVRDID	317

RESULT 2

AAW69957

ID AAW69957 standard; protein; 317 AA.

XX

AC AAW69957;

XX

DT 08-OCT-1998 (first entry)

XX

DE NF-kB receptor activator RANK ligand (RANKL).

XX

KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;

KW immune response; inflammatory response; toxic shock; sepsis; RANKL;

KW RANK ligand; tumour necrosis factor; TNF.

XX

OS Homo sapiens.

XX

PN WO9828426-A2.

XX

PD 02-JUL-1998.

XX

PF 22-DEC-1997; 97WO-US023775.

XX

PR 23-DEC-1996; 96US-0059978P.

PR 07-MAR-1997; 97US-00813509.

PR 14-OCT-1997; 97US-0064671P.

XX

PA (IMMV ) IMMUNEX CORP.

XX

PI Anderson DM, Galibert LJ, Maraskovsky E;

XX

DR WPI; 1998-377657/32.

DR N-PSDB; AAV41378.

XX

PT New isolated ligand for receptor activator of NF-kappa B - used to

PT develop products for augmenting an immune response for inhibiting an

PT inflammatory response and for protection of cells.

XX

PS Claim 27; Page 59-60; 80pp; English.

XX



```
DT      08-OCT-1998   (first entry)
XX
DE      NF-kB receptor activator RANK ligand (RANKL).
XX
KW      RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
KW      immune response; inflammatory response; toxic shock; sepsis; RANKL;
KW      RANK ligand; tumour necrosis factor; TNF.
XX
OS      Homo sapiens.
XX
PN      WO9828424-A2.
XX
PD      02-JUL-1998.
XX
PF      22-DEC-1997;    97WO-US023866.
XX
PR      23-DEC-1996;    96US-0059978P.
PR      07-MAR-1997;    97US-00813509.
PR      14-OCT-1997;    97US-0064671P.
XX
PA      (IMMV ) IMMUNEX CORP.
XX
PI      Anderson DM, Galibert LJ, Maraskovsky E;
XX
DR      WPI; 1998-377655/32.
DR      N-PSDB; AAV41372.
XX
PT      New isolated receptor activator of necrosis factor-kappa B - useful for,
PT      e.g. developing products for regulating an immune or inflammatory
PT      response, treating toxic shock or sepsis.
XX
PS      Example 7; Page 59-60; 80pp; English.
XX
CC      This represents a human RANKL, a ligand for the RANK (receptor activator
CC      of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a member of the
CC      tumour necrosis factor (TNF) family. Host cells transformed or
CC      transfected with an expression vector comprising the RANK encoding
CC      nucleic acid can be used to produce recombinant RANK protein. The soluble
CC      RANK may be used for inhibiting activation of NF-kB, by contacting a cell
CC      expressing membrane-associated RANK with a soluble RANK which binds to
CC      RANK ligand (RANKL). The soluble RANK polypeptide composition may also be
CC      used for regulating an immune or inflammatory response. Inhibition of NF-
CC      kB by RANK antagonists may be useful in ameliorating negative effects of
CC      an inflammatory response that result from triggering of RANK, e.g. in
CC      treating toxic shock or sepsis, graft-versus-host reactions, or acute
CC      inflammatory reactions. They can also be used in adjunct therapy for
CC      disease characterised by neoplastic cells that express RANK. The products
CC      can also be used for detection and drug screening
XX
SQ      Sequence 317 AA;

Query Match          100.0%; Score 1685; DB 2; Length 317;
Best Local Similarity 100.0%; Pred. No. 4.3e-154;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPAAASRSMFVALLGLGLGQV 60
        |||
```

Db	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV	60
Qy	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Db	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Qy	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH	180
Db	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH	180
Qy	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV	240
Db	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV	240
Qy	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEESISIEVSNPSLLD	300
Db	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEESISIEVSNPSLLD	300
Qy	301	PDQDATYFGAFKVRDID	317
Db	301	PDQDATYFGAFKVRDID	317

RESULT 4

AAE08738

ID AAE08738 standard; protein; 317 AA.

XX

AC AAE08738;

XX

DT 15-NOV-2001 (first entry)

XX

DE Human receptor activator of NF kappaB ligand (RANKL) protein.

XX

KW Human; receptor activator of nuclear factor kappaB ligand; RANKL; NF;

KW tumour necrosis factor; TNF; TNF receptor associated factor; TRAF;

KW immune response; inflammatory response; graft-versus-host reaction;

KW toxic shock; sepsis; acute inflammatory reaction; bone resorption;

KW anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory.

XX

OS Homo sapiens.

XX

PN US6271349-B1.

XX

PD 07-AUG-2001.

XX

PF 17-DEC-1998; 98US-00215649.

XX

PR 23-DEC-1996; 96US-0059978P.

PR 23-DEC-1996; 96US-00772330.

PR 07-MAR-1997; 97US-0077181P.

PR 07-MAR-1997; 97US-00813509.

PR 14-OCT-1997; 97US-0064671P.

PR 22-DEC-1997; 97US-00996139.

XX

PA (IMMV ) IMMUNEX CORP.

XX

PI Dougall WC, Galibert L;

XX  
DR WPI; 1998-377655/32.  
DR N-PSDB; AAD15311.  
XX  
PT New isolated receptor activator of necrosis factor-kappa B - useful for,  
PT e.g. developing products for regulating an immune or inflammatory  
PT response, treating toxic shock or sepsis.  
XX  
PS Example 15; Col 71-72; 47pp; English.  
XX  
CC The patent discloses novel receptor activator of nuclear factor (NF)-  
CC kappaB (RANK) proteins and their corresponding DNAs. RANK is a member of  
CC the tumour necrosis factor (TNF) receptor superfamily and associates with  
CC TNF receptor associated factor (TRAF) 2 and 3 which are important in the  
CC regulation of immune and inflammatory response. The receptors are useful  
CC for regulating immune response and in screening for inhibitors of these  
CC receptors. The cytoplasmic domain of RANK is used in developing assays  
CC for inhibitors of signal transduction, e.g. for screening the molecules  
CC that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3, TRAF5 and  
CC particularly TRAF6. NF-kappaB inhibition by RANK antagonists are useful  
CC in ameliorating the negative effects of an inflammatory response that  
CC result from triggering of RANK, e.g. in treating toxic shock or sepsis,  
CC graft-versus-host reactions, acute inflammatory reactions and the effects  
CC of bone resorption. RANK acts as an anti- apoptotic signal and rescue the  
CC cells that express RANK from apoptosis. Soluble forms of the receptor are  
CC used in vivo or in vitro based screening tests for agonists or  
CC antagonists of RANK activity, as antagonists of RANK-mediated NF-kappa B  
CC activation, or to inhibit transduction of a signal via RANK. RANK  
CC compositions are used in the development of both agonistic and  
CC antagonistic antibodies, or as an adjunct therapy for disease  
CC characterised by neoplastic cells that express RANK. Compounds that  
CC interfere with RANK/TRAF6 interactions are useful for modulating the  
CC formation of osteoclasts from osteoclast precursors and for modulating  
CC osteoclast function and activities. They are used as inhibitors of  
CC diseases associated with excess bone resorption and as immunosuppressants  
CC or anti-inflammatory agents. The RANK DNAs are useful for the expression  
CC of recombinant proteins, as probes for analysis of the presence or  
CC distribution of RANK transcripts, while the proteins are useful in  
CC preparing kits for the detection of soluble RANK, or monitor RANK-related  
CC activity. The present sequence is RANK ligand (RANKL) protein from human  
XX  
SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 2; Length 317;  
Best Local Similarity 100.0%; Pred. No. 4.3e-154;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
|  
Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
  
Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
|  
Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
  
Qy 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180  
|



Db 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180  
 QY 181 KVSLS SWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLMV 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 KVSLS SWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLMV 240  
 QY 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300  
 QY 301 PDQDATYFGAFKVRDID 317  
 ||||||||||||||||  
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 5

AA Y84417

ID AAY84417 standard; protein; 317 AA.

XX

AC AAY84417;

XX

DT 25-JUL-2000 (first entry)

XX

DE Amino acid sequence of a human osteoprotegerin ligand (OPGL).

XX

KW Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;

KW tumour necrosis factor receptor; type II transmembrane protein;

KW osteoclast differentiation; CSF-1; osteoclast activator; immune response;

KW osteoporosis; bone resorption.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 49. .69

FT /note= "transmembrane region"

FT Domain 70. .157

FT /note= "extracellular stalk domain"

FT Region 158. .317

FT /note= "active ligand moiety"

XX

PN WO200015807-A1.

XX

PD 23-MAR-2000.

XX

PF 13-SEP-1999; 99WO-DK000481.

XX

PR 15-SEP-1998; 98DK-00001164.

PR 02-OCT-1998; 98US-0102896P.

XX

PA (MEBI-) M & E BIOTECH AS.

XX

PI Halkier T, Haaning J;

XX

DR WPI; 2000-271444/23.

DR N-PSDB; AAZ99964.

XX

PT In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used to

PT treat, prevent and ameliorate osteoporosis.

XX

PS Claim 19; Page 78-79; 110pp; English.

XX

CC The present sequence represents a human osteoprotegerin ligand (OPGL).  
CC Osteoprotegerin is a secreted member of the tumour necrosis factor  
CC receptor family, which blocks osteoclastogenesis in a dose dependent  
CC manner. The OPGL protein is synthesised as a type II transmembrane  
CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL  
CC is a potent osteoclast differentiation factor when combined with CSF-1.  
CC It is not capable of inducing osteoclast differentiation in the absence  
CC of CSF-1. OPGL is also an activator of mature osteoclasts. The  
CC specification describes a method for the in vivo down-regulation of OPGL  
CC activity in an animal. The method comprises using at least one OPGL  
CC polypeptide or subsequence, and/or at least one OPGL analogue to induce  
CC an immune response in the animal. The method and OPGL polypeptide are  
CC useful for treating, preventing and ameliorating osteoporosis or other  
CC diseases or conditions characterised by excessive bone resorption

XX

SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 3; Length 317;  
Best Local Similarity 100.0%; Pred. No. 4.3e-154;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV	60
Db	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV	60
Qy	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Db	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Qy	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFahlTINATDIPSGSH	180
Db	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFahlTINATDIPSGSH	180
Qy	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV	240
Db	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV	240
Qy	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESISIEVSNPSLLD	300
Db	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESISIEVSNPSLLD	300
Qy	301	PDQDATYFGAFKVRDID	317
Db	301	PDQDATYFGAFKVRDID	317

RESULT 6

AAE04426

ID AAE04426 standard; protein; 317 AA.

XX

AC AAE04426;

XX

DT 04-SEP-2001 (first entry)

```

XX      Human receptor activator of NF-chi B ligand (huRANKL) protein.
XX
KW      Human; receptor activator of NF-chi B; RANK; tumour necrosis factor; TNF;
KW      CD40; TNF receptor-associated factor; TRAF; ligand; immune response;
KW      chromosome 18q22.1; huRANKL; chromosome 13q14; transmembrane protein.
XX
OS      Homo sapiens.
XX
FH      Key                Location/Qualifiers
FT      Region            162. .317
FT                        /note= "Receptor binding region"
XX
PN      US6242213-B1.
XX
PD      05-JUN-2001.
XX
PF      22-DEC-1997;      97US-00995659.
XX
PR      23-DEC-1996;      96US-0059978P.
PR      23-DEC-1996;      96US-00772330.
PR      07-MAR-1997;      97US-0077181P.
PR      14-OCT-1997;      97US-0064671P.
XX
PA      (IMMV ) IMMUNEX CORP.
XX
PI      Anderson DM;
XX
DR      WPI; 2001-407216/43.
DR      N-PSDB; AAD08715.
XX
PT      New DNA molecules, useful for producing ligands (which are useful for
PT      regulating immune response and in screening for inhibitors of NF-chi B
PT      receptor activator) of the receptor activator of NF-chi B (RANK).
XX
PS      Claim 1; Col 65-66; 43pp; English.
XX
CC      The present invention relates to receptor activator of NF-chi B (RANK)
CC      DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to
CC      chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane
CC      proteins respectively. RANK is a member of the tumour necrosis factor
CC      (TNF) superfamily and it closely resembles CD40 in the extracellular
CC      region. RANK associates with TNF receptor-associated factor (TRAF) 2 and
CC      TRAF3. The DNA molecules are useful for producing ligands of RANK. The
CC      ligands are useful for regulating immune response and in screening for
CC      inhibitors of RANK. The present sequence is human RANKL (huRANKL) protein
XX
SQ      Sequence 317 AA;

Query Match                100.0%;  Score 1685;  DB 4;  Length 317;
Best Local Similarity      100.0%;  Pred. No. 4.3e-154;
Matches 317;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

```

Qy	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Db	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Qy	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH	180
Db	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH	180
Qy	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQMV	240
Db	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQMV	240
Qy	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESIEVSNPSLLD	300
Db	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESIEVSNPSLLD	300
Qy	301	PDQDATYFGAFKVRDID	317
Db	301	PDQDATYFGAFKVRDID	317

RESULT 7

AAE01993

ID AAE01993 standard; protein; 317 AA.

XX

AC AAE01993;

XX

DT 31-JUL-2001 (first entry)

XX

DE Human full-length RANKL (receptor activator of NF-kappaB ligand).

XX

KW Human; receptor activator of NF-kappaB; RANK; nuclear factor-kappaB;  
 KW NF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein;  
 KW TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopathic;  
 KW inflammatory reaction; bone resorption; gene therapy; immunomodulator;  
 KW immune system dysfunction; familial expansile osteolysis; FEO;  
 KW early onset Paget's disease of bone; EP; cytostatic; chromosome 13q14.

XX

OS Homo sapiens.

XX

PN WO200136637-A1.

XX

PD 25-MAY-2001.

XX

PF 14-NOV-2000; 2000WO-US031459.

XX

PR 17-NOV-1999; 99US-00442029.

XX

PA (IMMV ) IMMUNEX CORP.

XX

PI Anderson DM, Hughes AE;

XX

DR WPI; 2001-329222/34.

DR

N-PSDB; AAD05904.

XX

PT New DNA encoding a receptor activator of NF-kappaB polypeptide for the  
 PT treatment of Pagets disease and Familial Expansile Osteolysis (FEO).

XX  
PS Disclosure; Page 76-77; 96pp; English.

XX  
CC The present invention relates to a novel receptor, referred to as RANK  
CC (receptor activator of NF (nuclear factor)-kappaB), a member of TNF  
CC (tumour necrosis factor) receptor superfamily. RANK is a Type I  
CC transmembrane protein that interacts with TNF receptor-associated factors  
CC (TRAFs). Triggering of RANK by overexpression or co-expression of RANK  
CC and membrane bound RANK ligand (RANKL) results in upregulation of the  
CC transcription factor NF-kappaB, a ubiquitous transcription factor that is  
CC most extensively utilised in cells of the immune system. Inhibition of NF  
CC -kappaB by RANK antagonists is useful in ameliorating negative effects of  
CC inflammatory reactions, and the effects of excess bone resorption. The  
CC RANK DNAs, proteins and their analogues are useful for the preparation of  
CC pharmaceutical compositions, for infecting target cells for use in gene  
CC therapy applications in diagnosing diseases associated with RANK, and as  
CC targets for use in screening assays. They may be used in the treatment or  
CC diagnosis of immune system dysfunction. The present invention also  
CC encompasses gene therapy methods to correct gene-activating mutations,  
CC associated with e.g. familial expansile osteolysis (FEO) and early onset  
CC Paget's disease of bone (EP). The present amino acid sequence is full-  
CC length human RANKL (huRANKL) protein. The RANKL gene is located in  
CC chromosome 13q14

XX  
SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 4; Length 317;  
Best Local Similarity 100.0%; Pred. No. 4.3e-154;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
|  
Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
  
Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
|  
Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
  
Qy 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFahlTINATDIPSGSH 180  
|  
Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFahlTINATDIPSGSH 180  
  
Qy 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240  
|  
Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240  
  
Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESIEVSNPSLLD 300  
|  
Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESIEVSNPSLLD 300  
  
Qy 301 PDQDATYFGAFKVRDID 317  
|  
Db 301 PDQDATYFGAFKVRDID 317

RESULT 8  
ABB08134

ID ABB08134 standard; protein; 317 AA.  
XX  
AC ABB08134;  
XX  
DT 10-SEP-2002 (first entry)  
XX  
DE Human RANKL polypeptide.  
XX  
KW Dendritic cell; mobilisation factor; T cell; adjuvant; antibacterial;  
KW fungicide; protozoacide; virucide; anti-inflammatory; anti-HIV;  
KW tuberculostatic; cytostatic; human; RANKL.  
XX  
OS Homo sapiens.  
XX  
PN WO200236141-A2.  
XX  
PD 10-MAY-2002.  
XX  
PF 30-OCT-2001; 2001WO-US044834.  
XX  
PR 02-NOV-2000; 2000US-0245721P.  
XX  
PA (IMMV ) IMMUNEX CORP.  
XX  
PI Lynch DH, De Smedt TN, Maliszewski CR, Butz EA, Miller RE;  
PI Thomas EK;  
XX  
DR WPI; 2002-500114/53.  
XX  
PT Treating an individual suffering from infection, e.g. inflammation,  
PT chickenpox or AIDS, by administering a combination of dendritic cell  
PT mobilization factor or maturation agent, T cell enhancing factor and  
PT antigen-specific T cells.  
XX  
PS Disclosure; Page 42-43; 43pp; English.  
XX  
CC The invention relates to treating an individual at risk for or suffering  
CC from infection with a pathogenic or opportunistic organism. The method  
CC involves administering a combination of two to five agents comprising:  
CC (a) dendritic cell mobilisation factor; (b) dendritic cell maturation  
CC agent; (c) dendritic cell activation agent; (d) T cell enhancing factor;  
CC or (e) activated, antigen-specific T cells. The methods are useful for  
CC treating an individual at risk for or suffering from infection with a  
CC pathogenic or opportunistic organism, e.g. viruses (e.g. HIV), bacteria  
CC (e.g. M. tuberculosis), yeast, fungi (e.g. C. albicans) or protozoa (e.g.  
CC T. cruzi, which causes Chaga's disease). The methods are especially  
CC useful for treating an individual suffering from immunosuppression by  
CC enhancing a lymphocyte-mediated immune response. In particular, the  
CC method is useful for treating inflammations, chickenpox, oral or genital  
CC herpes, mononucleosis, multifocal leukoencephalopathy, hepatitis, AIDS, T  
CC cell leukemia or T cell lymphoma. The activated antigen-presenting  
CC dendritic cells are useful as a vaccine adjuvant. The present sequence  
CC represents a human RANKL polypeptide fragment  
XX  
SQ Sequence 317 AA;

Query Match

100.0%; Score 1685; DB 5; Length 317;

Best Local Similarity 100.0%; Pred. No. 4.3e-154;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDIAKRSKLEAQPFAHLTINATDIPSGSH 180
        |||
Db    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDIAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240
        |||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300
        |||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
        |||
Db    301 PDQDATYFGAFKVRDID 317
```

RESULT 9

AAE26103

ID AAE26103 standard; protein; 317 AA.

XX

AC AAE26103;

XX

DT 14-NOV-2002 (first entry)

XX

DE Human RANK ligand (RANKL) protein.

XX

KW Human; RANK; receptor activator of nuclear factor-kappaB; NF-kB; sepsis;

KW immune response; toxic shock; graft-versus-host reaction; therapy; TRAF;

KW tumour necrosis factor receptor-associated factor; immunosuppressive;

KW antibacterial; antiinflammatory; chromosome 13.

XX

OS Homo sapiens.

XX

PN US2002086827-A1.

XX

PD 04-JUL-2002.

XX

PF 30-MAY-2001; 2001US-00871291.

XX

PR 23-DEC-1996; 96US-0059978P.

PR 07-MAR-1997; 97US-0077181P.

PR 14-OCT-1997; 97US-0064671P.

PR 22-DEC-1997; 97US-00996139.

PR 17-DEC-1999; 99US-00466496.

PR 24-MAY-2000; 2000US-00577800.

XX  
PA (IMMV ) IMMUNEX CORP.  
XX  
PI Anderson DM;  
XX  
DR WPI; 2002-642254/69.  
DR N-PSDB; AAD43213.  
XX  
PT A novel RANK (receptor activator of nuclear factor-kappaB (NF-kB))  
PT polypeptide, useful for inhibiting activation of NF-kB and for regulating  
PT an immune or inflammatory response in an individual.  
XX  
PS Example 15; Page 35; 49pp; English.  
XX  
CC The invention relates to novel RANK (receptor activator of nuclear factor  
CC -kappaB (NF-kB)) proteins and polynucleotides encoding them. Sequences of  
CC the invention are useful for inhibiting activation of NF-kappaB. They are  
CC useful for regulating an immune or inflammatory response in an individual  
CC at risk for an immune or inflammatory response. Inhibition of NF-kappaB  
CC by RANK antagonists is useful in ameliorating negative effects of an  
CC inflammatory response that results from triggering of RANK, for e.g. in  
CC treating toxic shock or sepsis, graft-versus-host reactions or acute  
CC inflammatory reactions. Soluble RANK is useful as an adjunct therapy for  
CC diseases characterised by neoplastic cells that express RANK. Soluble  
CC forms of the receptor are useful in vitro to screen for agonists or  
CC antagonists of RANK activity. The cytoplasmic domain of RANK is useful in  
CC developing assays for inhibitors of signal transduction, to screen for  
CC molecules that inhibit interaction of RANK with tumour necrosis factor  
CC receptor-associated factor (TRAF) 2 or TRAF3. The present sequence is  
CC human RANK ligand (RANKL) protein. RANKL gene is located on chromosome 13  
XX  
SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 5; Length 317;  
Best Local Similarity 100.0%; Pred. No. 4.3e-154;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHPQPPAASRSMFVALLGLGLGQV 60  
|  
Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHPQPPAASRSMFVALLGLGLGQV 60  
  
Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
|  
Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
  
Qy 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHLTINATDIPSGSH 180  
|  
Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHLTINATDIPSGSH 180  
  
Qy 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240  
|  
Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240  
  
Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300  
|  
Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300



Qy 301 PDQDATYFGAFKVRDID 317  
| | | | |  
Db 301 PDQDATYFGAFKVRDID 317

RESULT 10

ABG31631

ID ABG31631 standard; protein; 317 AA.

XX

AC ABG31631;

XX

DT 29-NOV-2002 (first entry)

XX

DE Human RANKL protein.

XX

KW Tumour; cancer; dendritic cell mobilisation factor; tumour-killing agent;

KW dendritic cell maturation agent; T cell enhancing factor; skin cancer;

KW antigen-specific T cell; prostate cancer; liver cancer; bone tumour;

KW brain tumour; spinal cord tumour; cervical intraepithelial neoplasia;

KW actinic keratosis; dendritic cell maturation stimulator; cytostatic;

KW dendritic cell activator; T cell enhancer; human; RANKL.

XX

OS Homo sapiens.

XX

PN WO200266044-A2.

XX

PD 29-AUG-2002.

XX

PF 23-OCT-2001; 2001WO-US046254.

XX

PR 24-OCT-2000; 2000US-0242868P.

XX

PA (IMMV ) IMMUNEX CORP.

XX

PI Thomas EK, Lyman SD, Lynch DH, De Smedt TN, Maliszewski CR;

XX

DR WPI; 2002-674891/72.

XX

PT Treating an individual with tumors or cancers, e.g. liver cancer or brain

PT tumor, by administering a combination of dendritic cell populations, T

PT cell enhancing factors and activated, antigen-specific T cells.

XX

PS Disclosure; Page 43-44; 44pp; English.

XX

CC The present invention relates to a new method for treating a tumour-  
CC bearing subject. The method involves administering a combination of 2 to  
CC 5 agents comprising dendritic cell mobilisation factor, dendritic cell  
CC maturation agent, tumour-killing agent, T cell enhancing factor or  
CC activated, antigen-specific T cells. The method is useful for treating  
CC tumours or cancers in a subject e.g. skin cancer, prostate cancer, liver  
CC cancer, tumours of the bone, brain or spinal cord, actinic keratosis, or  
CC cervical intraepithelial neoplasia. The present amino acid sequence  
CC represents the human RANKL protein that was used in the method of the  
CC invention

XX

SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 5; Length 317;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-154;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
      |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

QY     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
      |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

QY    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAPHLTINATDIPSGSH 180
      |||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAPHLTINATDIPSGSH 180

QY    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
      |||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

QY    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEIEISIEVSNPSLLD 300
      |||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEIEISIEVSNPSLLD 300

QY    301 PDQDATYFGAFKVRDID 317
      |||
Db    301 PDQDATYFGAFKVRDID 317
  
```

RESULT 11

AAU78285

ID AAU78285 standard; protein; 317 AA.

XX

AC AAU78285;

XX

DT 18-JUN-2002 (first entry)

XX

DE Human TRANCE protein splice variant 1.

XX

KW Human; tumour necrosis factor-related activation induced cytokine;

KW TRANCE; dwarfism; osteopetrosis; craniofacial-skeletal discrepancy;

KW bone damage; cartilage damage; traumatic injury; surgery; osteoarthritis;

KW rheumatoid arthritis; acromegaly; gigantism; exostosis; carilaginea;

KW exostosis bursata; multiple osteocartilaginous exostosis; chondrocyte;

KW cartilage growth; skeletal growth.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 126. .317

FT /note= "Specifically claimed in claims 17 and 18"

FT Region 137. .317

FT /note= "Specifically claimed in claims 17 and 18"

FT Region 140. .317

FT /note= "Specifically claimed in claims 17 and 18"

FT Region 145. .317

FT /note= "Specifically claimed in claims 17 and 18"

FT Region 158. .317  
 FT /note= "Specifically claimed in claims 17 and 18"  
 FT Domain 159. .317  
 FT /note= "TNF core domain, specifically claimed in claims  
 FT 17 and 18"  
 XX  
 PN WO200216551-A2.  
 XX  
 PD 28-FEB-2002.  
 XX  
 PF 20-AUG-2001; 2001WO-US026101.  
 XX  
 PR 18-AUG-2000; 2000US-0226197P.  
 XX  
 PA (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.  
 XX  
 PI Choi Y, Odgren PR, Marks SC;  
 XX  
 DR WPI; 2002-304119/34.  
 DR N-PSDB; ABK12876.  
 XX  
 PT Treating mammal having disorder characterized by abnormal  
 PT cartilage/skeletal growth such as dwarfism, acromegaly, by administering  
 PT tumor necrosis factor-related activation induced cytokine-modulating  
 PT agent to mammal.  
 XX  
 PS Disclosure; Fig 10; 55pp; English.  
 XX  
 CC The present invention relates to a new method of treating a mammal having  
 CC a disorder comprising insufficient or excessive cartilage or skeletal  
 CC growth. The method of the invention involves administering to the mammal  
 CC a tumour necrosis factor-related activation induced cytokine (TRANCE)-  
 CC modulating agent. The method is useful for treating a mammal having a  
 CC disorder comprising insufficient or excessive cartilage or skeletal  
 CC growth, where the disorder comprising insufficient cartilage or skeletal  
 CC growth is selected from dwarfism, osteopetrosis, craniofacial-skeletal  
 CC discrepancies and bone or cartilage damage resulting from traumatic  
 CC injury, surgery, osteoarthritis or rheumatoid arthritis, and disorders  
 CC comprising excessive cartilage or skeletal growth are selected from  
 CC acromegaly, gigantism, exostosis, carilaginea, exostosis bursata and  
 CC multiple osteocartilaginous exostoses. The method is useful for  
 CC inhibiting chondrocyte differentiation. The present amino acid sequence  
 CC represents the human TRANCE protein, splice variant 1, of the invention.  
 CC TRANCE is a member of the tumour necrosis factor family and acts directly  
 CC on cartilage-producing cells (chondrocytes)  
 XX  
 SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 5; Length 317;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-154;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMEVALLGLGLGQV 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMEVALLGLGLGQV 60  
 Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

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      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy      121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

Qy      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESISIEVSNPSLLD 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESISIEVSNPSLLD 300

Qy      301 PDQDATYFGAFKVRDID 317
      ||||||||||||||||
Db      301 PDQDATYFGAFKVRDID 317

```

RESULT 12

AAO19096

ID AAO19096 standard; protein; 317 AA.

XX

AC AAO19096;

XX

DT 22-NOV-2002 (first entry)

XX

DE C neoformans antigen expressing dendritic cell related protein #5.

XX

KW Human; fungicide; fungal infection; dendritic cell; antigen;

KW Cryptococcus neoformans; vaccine; immunostimulant.

XX

OS Homo sapiens.

XX

PN WO200266053-A2.

XX

PD 29-AUG-2002.

XX

PF 14-DEC-2001; 2001WO-US048288.

XX

PR 04-JAN-2001; 2001US-0259653P.

XX

PA (IMMV ) IMMUNEX CORP.

XX

PI Thomas EK;

XX

DR WPI; 2002-674896/72.

XX

PT Producing a population of activated, Cryptococcus neoformans antigen-

PT presenting dendritic cells for preventing or treating C. neoformans

PT infection comprises causing the obtained dendritic cells to present the

PT antigen.

XX

PS Disclosure; Page 30-32; 32pp; English.

XX

CC The present invention relates to a method of producing a population of

CC activated, Cryptococcus neoformans antigen-presenting dendritic cells,  
CC comprising causing the obtained dendritic cells to present the antigen  
CC and maturing the dendritic cells. The activated, C. neoformans antigen-  
CC expressing dendritic cells are useful for treating, or as vaccines or  
CC vaccine adjuvants against, C. neoformans infection, or for generating  
CC antigen-specific T cells. The present sequence is a human protein shown  
CC in the exemplification of the invention

XX

SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 5; Length 317;  
Best Local Similarity 100.0%; Pred. No. 4.3e-154;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
          |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
          |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180
          |||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240
          |||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
          |||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
          |||
Db    301 PDQDATYFGAFKVRDID 317
```

#### RESULT 13

ABP55108

ID ABP55108 standard; protein; 317 AA.

XX

AC ABP55108;

XX

DT 05-FEB-2003 (first entry)

XX

DE Human osteoprotegerin ligand.

XX

KW Osteoprotegerin ligand; OPG ligand; OPGL; human; autoimmune disease;

KW rheumatoid arthritis; diabetes; osteoarthritis; psoriasis;

KW inflammatory bowel disease; transplant rejection; allergy;

KW immunosuppressive; antirheumatic; antiarthritic; antidiabetic;

KW antipsoriatic; immunosuppressive; antiallergic; antiinflammatory;

KW osteopathic; antiulcer; monocyte.

XX

OS Homo sapiens.

XX  
FH Key Location/Qualifiers  
FT Domain 1. .47  
FT /note= "putative cytoplasmic domain"  
FT Domain 48. .68  
FT /note= "putative transmembrane signal-anchor"  
FT Domain 69. .317  
FT /note= "putative extracellular domain"  
FT Modified-site 171  
FT /note= "potential N-glycosylation site"  
FT Modified-site 198  
FT /note= "potential N-glycosylation site"  
XX  
PN WO200276507-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 06-FEB-2002; 2002WO-US001238.  
XX  
PR 23-MAR-2001; 2001US-0278215P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Grewal I;  
XX  
DR WPI; 2003-058352/05.  
DR N-PSDB; ABV75842.  
XX  
PT Stimulating mammalian monocytes by exposing to an OPG ligand polypeptide,  
PT useful for treating immune related disorders such as autoimmune disease,  
PT rheumatoid arthritis, diabetes, osteoarthritis, psoriasis, and allergy.  
XX  
PS Claim 1; Fig 1B; 111pp; English.  
XX  
CC The present sequence is the protein sequence of human osteoprotegerin  
CC ligand (OPGL), a member of the tumour necrosis factor (TNF) family of  
CC molecules that has been reported to bind to at least 2 receptors, RANK  
CC and OPG. In the present invention, OPGL was shown to activate human  
CC monocytes, and to activate such monocytes to secrete certain cytokines  
CC such as interleukin-1 (IL-1), IL-6, IL-12, MIP-1alpha and TNF-alpha and  
CC chemokines such as IL-8. OPGL may function in up-regulation of co-  
CC stimulatory molecules such as ICAM-a and VCAM-1, LFA, and B7.1, B7.3 and  
CC B7h. OPGL may also serve as an antigen presenting molecule which enhances  
CC T-cell activation. The invention provides methods of using OPGL to  
CC activate monocytes to secrete chemokines or cytokines by exposing a  
CC mammalian cell (in cell culture or in a mammal) to OPGL. Also provided  
CC are methods of using OPGL to treat conditions or diseases in mammals  
CC associated with, or resulting from lack of, or decreased, chemokine or  
CC cytokine secretion by monocytes. The invention also provides agonist and  
CC antagonist molecules to modulate immune activity. These may include  
CC antibodies to the OPG or RANK receptors. An antagonist comprising an anti  
CC -OPGL antibody, an anti-OPG receptor antibody, an anti-RANK receptor  
CC antibody, an OPG receptor immunoadhesin or a RANK receptor immunoadhesin  
CC is used in a claimed method of treating an immune-related condition,  
CC especially an autoimmune disease, rheumatoid arthritis, insulin dependent  
CC diabetes, osteoarthritis, inflammatory bowel disease (especially  
CC ulcerative colitis or Crohn's disease), psoriasis, transplant rejection

CC or allergy  
XX  
SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 6; Length 317;  
Best Local Similarity 100.0%; Pred. No. 4.3e-154;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

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Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAPHLTINATDIPSGSH 180

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Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESIEVSNPSLLD 300
          |||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
          |||
Db    301 PDQDATYFGAFKVRDID 317
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RESULT 14

AAE34364

ID AAE34364 standard; protein; 317 AA.

XX

AC AAE34364;

XX

DT 14-MAY-2003 (first entry)

XX

DE Human receptor activator of NF-kappa B ligand (RANKL).

XX

KW Human; acute septic arthritis; osteomalacia; hyperparathyroidism;

KW Cushing's syndrome; receptor activator of NF-kappa B ligand; cancer;

KW bone formation; rickets; Langerhan's cell histiocytosis; gene therapy;

KW monoostotic fibrous dysplasia; radiation therapy; spinal cord injury;

KW RANKL; Gaucher's disease; polyostotic fibrous dysplasia; scurvy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 1. .47

FT /note= "Intracellular domain"

FT Domain 48. .68

FT /note= "Transmembrane domain"

FT Domain 69. .317

FT /note= "Extracellular domain"  
 FT Binding-site 162. .317  
 FT /note= "RANK-binding domain"  
 XX  
 PN WO200292016-A2.  
 XX  
 PD 21-NOV-2002.  
 XX  
 PF 17-MAY-2002; 2002WO-US016002.  
 XX  
 PR 17-MAY-2001; 2001US-0291919P.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 PI Dougall WC, Anderson DM;  
 XX  
 DR WPI; 2003-129220/12.  
 DR N-PSDB; AAD52598.  
 XX  
 PT Treating patients having e.g. acute septic arthritis, osteomalacia,  
 PT hyperparathyroidism, Cushing's syndrome or spinal cord injury, comprises  
 PT administering a receptor activator of NF-kappa B antagonist to increase  
 PT bone formation.  
 XX  
 PS Claim 1; Page 51-52; 52pp; English.  
 XX  
 CC The invention relates to a method of treating a patient having e.g. acute  
 CC septic arthritis, osteomalacia, hyperparathyroidism, Cushing's syndrome  
 CC or spinal cord injury. The method involves administering a receptor  
 CC activator of NF-kappa B (RANK) antagonist to stimulate an increase in the  
 CC rate for formation of new bone. RANK antagonist is capable of inhibiting  
 CC the ability of RANK to induce NF-kappa B. The method is useful for  
 CC stimulating bone formation, or for treating patients having acute septic  
 CC arthritis, osteomalacia (including rickets and scurvy),  
 CC hyperparathyroidism, Cushing's syndrome, monoostotic fibrous dysplasia,  
 CC polyostotic fibrous dysplasia, Gaucher's disease, Langerhan's cell  
 CC histiocytosis, spinal cord injury, patients requiring periodontal  
 CC reconstruction, or patients who have completed a course or radiation  
 CC therapy for cancer. The method is also useful for treating a patient who  
 CC is a prosthetic joint recipient, a bone graft recipient, or a ligament  
 CC graft recipient. The invention is useful in gene therapy. The present  
 CC sequence is human RANK ligand (RANKL) protein  
 XX  
 SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 6; Length 317;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-154;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120



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Db	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF	180
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RESULT 15

ABR42314

ID ABR42314 standard; protein; 317 AA.

XX

AC ABR42314;

XX

DT 11-AUG-2003 (first entry)

XX

DE Human RANKL protein.

XX

KW Human; RANKL; tumour necrosis factor; ligand; cytostatic;

KW immunomodulator; osteopathic.

XX

OS Homo sapiens.

XX

PN WO2003040307-A2.

XX

PD 15-MAY-2003.

XX

PF 25-JUL-2002; 2002WO-US023782.

XX

PR 27-JUL-2001; 2001US-0307838P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Hilbert DH, Rosen CA;

XX

DR WPI; 2003-430659/40.

XX

PT New heteromultimeric complex having a first polypeptide member of the  
PT tumor necrosis factor (TNF) ligand family, and a second different member  
PT of TNF ligand family, useful for treating cancer, osteoporosis or an  
PT autoimmune disease.

XX

PS Disclosure; Page 366-367; 388pp; English.

XX

CC The present sequence is the protein sequence of human RANKL protein. The  
CC invention relates to compositions comprising heterotrimeric complexes of  
CC tumour necrosis factor (TNF) ligand family members, and their use in the  
CC detection, prevention and treatment of disease. In one embodiment, the

CC heterotrimeric complex comprises full-length or extracellular portions of  
CC RANKL and full-length or extracellular portions of other TNF ligand  
CC family members, preferably TRAIL. The heterotrimeric complexes of the  
CC invention are useful for treating an autoimmune disease, cancer or  
CC osteoporosis, and particularly for inhibiting cancer cell proliferation,  
CC increasing B cell proliferation, or inducing apoptosis of T cells. A  
CC claimed method of inhibiting cancer cell proliferation comprises  
CC administering a heterotrimeric complex consisting of TRAIL and CD40L or  
CC RANKL. A claimed method of treating osteoporosis comprises administering  
CC an antibody against a complex comprising RANKL and TRAIL  
XX  
SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 6; Length 317;  
Best Local Similarity 100.0%; Pred. No. 4.3e-154;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHTINATDIPSGSH 180  
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Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHTINATDIPSGSH 180  
  
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Job time : 129 secs

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Scoring table: BLOSUM62  
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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
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 and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	1685	100.0	317	3	US-09-215-649A-13	Sequence 13, Appl
4	1685	100.0	317	4	US-09-052-521C-4	Sequence 4, Appli
5	1685	100.0	317	4	US-09-577-780-13	Sequence 13, Appl
6	1685	100.0	317	4	US-09-577-800-13	Sequence 13, Appl
7	1685	100.0	317	4	US-09-466-496-13	Sequence 13, Appl
8	1685	100.0	317	4	US-09-871-856-13	Sequence 13, Appl
9	1685	100.0	317	4	US-09-871-291-13	Sequence 13, Appl
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11	1685	100.0	317	4	US-09-877-650-13	Sequence 13, Appl

12	1417.5	84.1	316	2	US-08-842-842-7	Sequence 7, Appli
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15	1417.5	84.1	316	4	US-09-671-658A-2	Sequence 2, Appli
16	1417.5	84.1	316	4	US-09-396-937-4	Sequence 4, Appli
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18	1326.5	78.7	294	3	US-08-996-139-11	Sequence 11, Appl
19	1326.5	78.7	294	3	US-08-995-659-11	Sequence 11, Appl
20	1326.5	78.7	294	3	US-09-215-649A-11	Sequence 11, Appl
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22	1326.5	78.7	294	4	US-09-577-800-11	Sequence 11, Appl
23	1326.5	78.7	294	4	US-09-466-496-11	Sequence 11, Appl
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25	1326.5	78.7	294	4	US-09-871-291-11	Sequence 11, Appl
26	1326.5	78.7	294	4	US-09-877-650-11	Sequence 11, Appl
27	771	45.8	187	4	US-09-396-937-8	Sequence 8, Appli
28	769	45.6	173	4	US-09-396-937-10	Sequence 10, Appl
29	759	45.0	173	4	US-09-396-937-12	Sequence 12, Appl
30	721.5	42.8	188	4	US-09-396-937-14	Sequence 14, Appl
31	711.5	42.2	182	4	US-09-396-937-16	Sequence 16, Appl
32	691	41.0	173	4	US-09-396-937-18	Sequence 18, Appl
33	670	39.8	173	4	US-09-396-937-20	Sequence 20, Appl
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39	251.5	14.9	281	3	US-08-780-496-1	Sequence 1, Appli
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43	251.5	14.9	281	4	US-09-157-864-11	Sequence 11, Appl
44	251.5	14.9	281	4	US-09-825-563-2	Sequence 2, Appli
45	251.5	14.9	281	4	US-10-039-785-66	Sequence 66, Appl

#### ALIGNMENTS

##### RESULT 1

US-08-996-139-13

; Sequence 13, Application US/08996139

; Patent No. 6017729

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; APPLICANT: Galibert, Laurent

; APPLICANT: Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-996-139-13

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Query Match          100.0%; Score 1685; DB 3; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.6e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

US-08-995-659-13

; Sequence 13, Application US/08995659

; Patent No. 6242213

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; APPLICANT: Galibert, Laurent

; APPLICANT: Maraskovsky, Eugene

; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/995,659

; FILING DATE: 22 DECEMBER 1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 60/064,671

; FILING DATE: 14 OCTOBER 1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/813,509

; FILING DATE: 07 MARCH 1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/772,330

; FILING DATE: 23 DECEMBER 1996

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia Anne

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2852-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206)587-0430

; TELEFAX: (206)233-0644

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 317 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-995-659-13

Query Match 100.0%; Score 1685; DB 3; Length 317;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-163;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

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# RESULT 3

US-09-215-649A-13

; Sequence 13, Application US/09215649A

; Patent No. 6271349

## ; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/215,649A

; FILING DATE: 17-Dec-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/996,139

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;          FILING DATE: <Unknown>
;          APPLICATION NUMBER: USSN 08/813,509
;          FILING DATE: 07 MARCH 1997
;          APPLICATION NUMBER: USSN 08/772,330
;          FILING DATE: 23 DECEMBER 1996
;    ATTORNEY/AGENT INFORMATION:
;          NAME: Perkins, Patricia Anne
;          REGISTRATION NUMBER: 34,693
;          REFERENCE/DOCKET NUMBER: 2851-A
;    TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (206)587-0430
;          TELEFAX: (206)233-0644
;    INFORMATION FOR SEQ ID NO: 13:
;          SEQUENCE CHARACTERISTICS:
;            LENGTH: 317 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;          MOLECULE TYPE: protein
;          SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-215-649A-13

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Query Match          100.0%;  Score 1685;  DB 3;  Length 317;
Best Local Similarity 100.0%;  Pred. No. 2.6e-163;
Matches 317;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHLTINATDIPSGSH 180
        |||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQMV 240
        |||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        |||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
        |||
Db    301 PDQDATYFGAFKVRDID 317

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#### RESULT 4

US-09-052-521C-4

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; Sequence 4, Application US/09052521C
; Patent No. 6316408
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors

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; FILE REFERENCE:  A-451Brv
; CURRENT APPLICATION NUMBER:  US/09/052,521C
; CURRENT FILING DATE:  1998-03-30
; PRIOR APPLICATION NUMBER:  08/880,855
; PRIOR FILING DATE:  1997-06-23
; PRIOR APPLICATION NUMBER:  08/842,842
; PRIOR FILING DATE:  1997-04-16
; NUMBER OF SEQ ID NOS:  40
; SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Human
US-09-052-521C-4
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Query Match          100.0%; Score 1685; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.6e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
          |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
          |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180
          |||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQMV 240
          |||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
          |||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
          |||
Db    301 PDQDATYFGAFKVRDID 317
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# RESULT 5

US-09-577-780-13

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; Sequence 13, Application US/09577780
; Patent No. 6419929
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## GENERAL INFORMATION:

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; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
```

```

;          CITY: Seattle
;          STATE: WA
;          COUNTRY: USA
;          ZIP: 98101
;
;  COMPUTER READABLE FORM:
;
;          MEDIUM TYPE: Floppy disk
;          COMPUTER: Apple Power Macintosh
;          OPERATING SYSTEM: Apple Operating System 7.5.5
;          SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;
;  CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/09/577,780
;          FILING DATE: 24-May-2000
;          CLASSIFICATION: <Unknown>
;
;  PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: 08/995,659
;          FILING DATE: <Unknown>
;          APPLICATION NUMBER: USSN 08/813,509
;          FILING DATE: 07 MARCH 1997
;          APPLICATION NUMBER: USSN 08/772,330
;          FILING DATE: 23 DECEMBER 1996
;
;  ATTORNEY/AGENT INFORMATION:
;          NAME: Perkins, Patricia Anne
;          REGISTRATION NUMBER: 34,693
;          REFERENCE/DOCKET NUMBER: 2852-A
;
;  TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (206)587-0430
;          TELEFAX: (206)233-0644
;
;  INFORMATION FOR SEQ ID NO: 13:
;          SEQUENCE CHARACTERISTICS:
;              LENGTH: 317 amino acids
;              TYPE: amino acid
;              TOPOLOGY: linear
;          MOLECULE TYPE: protein
;          SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-577-780-13

```

```

Query Match          100.0%;  Score 1685;  DB 4;  Length 317;
Best Local Similarity 100.0%;  Pred. No. 2.6e-163;
Matches 317;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGA VQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180
        |||
Db    121 QAFQGA VQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQLMV 240
        |||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

```

```

                ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEEISIEVSNPSLLD 300

Qy          301 PDQDATYFGAFKVRDID 317
                ||||||||||||||||
Db          301 PDQDATYFGAFKVRDID 317

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RESULT 6

US-09-577-800-13

; Sequence 13, Application US/09577800

; Patent No. 6479635

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; APPLICANT: Galibert, Laurent

; APPLICANT: Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/577,800

; FILING DATE: 24-MAY-2000

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/996,139

; FILING DATE: 22 DECEMBER 1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 60/064,671

; FILING DATE: 14 OCTOBER 1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/813,509

; FILING DATE: 07 MARCH 1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/772,330

; FILING DATE: 23 DECEMBER 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia Anne

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2851-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206)587-0430

; TELEFAX: (206)233-0644

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 317 amino acids

; TYPE: amino acid

; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-577-800-13

Query Match 100.0%; Score 1685; DB 4; Length 317;  
Best Local Similarity 100.0%; Pred. No. 2.6e-163;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV	60
Db	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV	60
Qy	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Db	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Qy	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFahlTinAtDiPSGSH	180
Db	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFahlTinAtDiPSGSH	180
Qy	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV	240
Db	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV	240
Qy	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHfYSINVGgFFKLRSgEEISIEVSNPSLLD	300
Db	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHfYSINVGgFFKLRSgEEISIEVSNPSLLD	300
Qy	301	PDQDATYFGAFKVRDID	317
Db	301	PDQDATYFGAFKVRDID	317

RESULT 7

US-09-466-496-13

; Sequence 13, Application US/09466496

; Patent No. 6528482

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/466,496

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;          FILING DATE: 17-Dec-1999
;          CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: US/08/996,139
;          FILING DATE: 22 DECEMBER 1997
;          APPLICATION NUMBER: USSN 60/064,671
;          FILING DATE: 14 OCTOBER 1997
;          APPLICATION NUMBER: USSN 08/813,509
;          FILING DATE: 07 MARCH 1997
;          APPLICATION NUMBER: USSN 08/772,330
;          FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
;          NAME: Perkins, Patricia Anne
;          REGISTRATION NUMBER: 34,693
;          REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (206)587-0430
;          TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-466-496-13

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Query Match          100.0%; Score 1685; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.6e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
        ||||||||||||||||
Db    301 PDQDATYFGAFKVRDID 317

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RESULT 8



Db	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Qy	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAPHLTINATDIPSGSH	180
Db	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAPHLTINATDIPSGSH	180
Qy	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV	240
Db	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV	240
Qy	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD	300
Db	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD	300
Qy	301	PDQDATYFGAFKVRDID	317
Db	301	PDQDATYFGAFKVRDID	317

RESULT 9

US-09-871-291-13

; Sequence 13, Application US/09871291

; Patent No. 6562948

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/871,291

; FILING DATE: 30-May-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/996,139

; FILING DATE: <Unknown>

; APPLICATION NUMBER: USSN 08/813,509

; FILING DATE: 07 MARCH 1997

; APPLICATION NUMBER: USSN 08/772,330

; FILING DATE: 23 DECEMBER 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia Anne

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2851-A

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-871-291-13

```

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Query Match          100.0%; Score 1685; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.6e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
|
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
|
Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
|
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
|
Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180
|
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180
|
Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240
|
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240
|
Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
|
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
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Qy    301 PDQDATYFGAFKVRDID 317
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Db    301 PDQDATYFGAFKVRDID 317

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# RESULT 10

US-09-396-937-2

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; Sequence 2, Application US/09396937
; Patent No. 6645500
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 22021 PC 1
; CURRENT APPLICATION NUMBER: US/09/396,937
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2

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;           APPLICATION NUMBER: US/09/877,650
;           FILING DATE: 08-Jun-2001
;           CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: 08/995,659
;           FILING DATE: 1997-12-22
;           APPLICATION NUMBER: USSN 08/813,509
;           FILING DATE: 07 MARCH 1997
;           APPLICATION NUMBER: USSN 08/772,330
;           FILING DATE: 23 DECEMBER 1996
;   ATTORNEY/AGENT INFORMATION:
;           NAME: Perkins, Patricia Anne
;           REGISTRATION NUMBER: 34,693
;           REFERENCE/DOCKET NUMBER: 2852-A
;   TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (206)587-0430
;           TELEFAX: (206)233-0644
;   INFORMATION FOR SEQ ID NO: 13:
;           SEQUENCE CHARACTERISTICS:
;             LENGTH: 317 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;           MOLECULE TYPE: protein
;           SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-877-650-13

```

```

Query Match          100.0%;  Score 1685;  DB 4;  Length 317;
Best Local Similarity 100.0%;  Pred. No. 2.6e-163;
Matches 317;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPPFAHLTINATDIPSGSH 180
        |||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPPFAHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
        |||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        |||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
        |||
Db    301 PDQDATYFGAFKVRDID 317

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RESULT 12  
 US-08-842-842-7

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; Sequence 7, Application US/08842842
; Patent No. 5843678
; GENERAL INFORMATION:
;   APPLICANT: Boyle, William J.
;   TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
;   NUMBER OF SEQUENCES: 7
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Amgen Inc.
;     STREET: 1840 Dehavilland Drive
;     CITY: Thousand Oaks
;     STATE: California
;     COUNTRY: USA
;     ZIP: 91230-1789
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/842,842
;     FILING DATE:
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Winter, Robert B.
;     REFERENCE/DOCKET NUMBER: A-451
; INFORMATION FOR SEQ ID NO: 7:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 316 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-842-842-7

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Query Match          84.1%; Score 1417.5; DB 2; Length 316;
Best Local Similarity 84.3%; Pred. No. 4.6e-136;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPPPAPHQPPAASRSMFVALLGLGLGQ 59
        ||||| |||| |||| ||| ||||| || ||| |||||:|||||
Db      1 MRRASRDYGKYLRSEEMGGSGPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ 60

Qy     60 VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI 119
        |||:||| ||||| ||||| ||| ||||| ||| ||:||||:| :|||:|
Db     61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESED--LPDSCRMM 118

Qy    120 KQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHTINATDIPSGS 179
        ||||| ||||| ||| |||:||||:|:| ||||| |||||
Db    119 KQAFQGAVQKELQHIVGPRFSGAPAMMEGSWLDVAQQRGKPEAQPFHAHTINAASIPSGS 178

Qy    180 HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLM 239
        |||:||||| ||||| ||||| ||||| ||||| ||||| :|:||||
Db    179 HKVTLSSWYHDRGWAKISNMTLSNGKLVRVNDGFYYLYANICFRHHETSGSVPTDYLQLM 238

Qy    240 VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFFKLRSGEEISIEVSNPSSL 299
        ||| ||||| ||||| ||||| ||||| ||||| |||||:||||:||||
Db    239 VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGFFFKLRAGEEISIQVSNPSSL 298

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Qy 300 DPDQDATYFGAFKVRDID 317  
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Db 299 DPDQDATYFGAFKVQDID 316

RESULT 13  
US-08-989-362-2  
; Sequence 2, Application US/08989362  
; Patent No. 6242586  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Mattson, Jeanine D.  
; TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related  
; TITLE OF INVENTION: Reagents  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/989,362  
; FILING DATE: 12-DEC-1997  
; CLASSIFICATION: 56  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/032,846  
; FILING DATE: 13-DEC-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0686  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650)852-9196  
; TELEFAX: (650)496-1204  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 316 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-989-362-2

Query Match 84.1%; Score 1417.5; DB 3; Length 316;  
Best Local Similarity 84.3%; Pred. No. 4.6e-136;  
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPAPHQPPAASRSMEVALLGLGLGQ 59  
||||||| |||| ||||| ||| ||||| || ||| |||||:|||||||  
Db 1 MRRASRDYGKYLRSSSEEMGSGPGVPHEGPLHPAPSAPAPAPPPAASRSMEFLALLGLGLGQ 60



Db 119 KQAFQGA VQKELQHIVGPQRFS GAPAMMEGSWLDVAQRGKPEAQPF AHLTINAASIPSGS 178  
 Qy 180 HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLM 239  
 |||:||||| ||||| ||||| ||||| ||||| : |:|||||  
 Db 179 HKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDY LQLM 238  
 Qy 240 VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNP SLL 299  
 ||| ||||| ||||| ||||| ||||| ||||| ||||| : ||||| : |||||  
 Db 239 VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKL RAGEEISIQVSNP SLL 298  
 Qy 300 DPDQDATYFGAFKVRDID 317  
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 Db 299 DPDQDATYFGAFKVQDID 316

RESULT 15

US-09-671-658A-2

; Sequence 2, Application US/09671658A

; Patent No. 6525180

; GENERAL INFORMATION:

; APPLICANT: Gorman, Daniel M.

; Mattson, Jeanine D.

; TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related

; Reagents

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DNAX Research Institute

; STREET: 901 California Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/671,658A

; FILING DATE: 27-Sep-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/989,362

; FILING DATE: 12-DEC-1997

; APPLICATION NUMBER: US 60/032,846

; FILING DATE: 13-DEC-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Ching, Edwin P.

; REGISTRATION NUMBER: 34,090

; REFERENCE/DOCKET NUMBER: DX0686

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650)852-9196

; TELEFAX: (650)496-1204

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 316 amino acids

; TYPE: amino acid

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;          TOPOLOGY: linear
;          MOLECULE TYPE: protein
;          SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-671-658A-2

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Query Match 84.1%; Score 1417.5; DB 4; Length 316;  
Best Local Similarity 84.3%; Pred. No. 4.6e-136;  
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

Qy	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPAPHPQPPAASRSMFVALLGLGLGQ	59
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Db	1	MRRASRDYGKYLRSSSEEMGSGPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ	60
Qy	60	VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI	119
		:                                :   :   :    :	
Db	61	VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESED--LPDSCRMM	118
Qy	120	KQAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGS	179
		:      : :	
Db	119	KQAFQGA VQKELQHIVGPQRFSGAPAMMEG SWLDVAQRGKPEAQPFALTINAASIPSGS	178
Qy	180	HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLM	239
		:  : :	
Db	179	HKVTLSSWYHDRGWAKISNMTLSNGKL RVNQDGFYYLYANICFRHHETSGSVPTDYLQLM	238
Qy	240	VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLL	299
		:     :	
Db	239	VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKL RAGEEISIQVSNPSLL	298
Qy	300	DPDQDATYFGAFKVRDID	317
		:	
Db	299	DPDQDATYFGAFKVQDID	316

Search completed: September 15, 2004, 08:34:22  
Job time : 36 secs

OM protein - protein search, using sw model

Run on: September 15, 2004, 08:32:22 ; Search time 40 Seconds  
 (without alignments)  
 762.318 Million cell updates/sec

Title: US-09-211-315-39  
 Perfect score: 1685  
 Sequence: 1 MRRASRDYTKYLRGSEEMGG.....LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR\_78:\*  
 1: pirl:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	% Query		Match Length	DB	ID	Description
	Score	Match				
1	189	11.2	281	2	I38707	Fas ligand - human
2	184.5	10.9	279	2	A53062	Fas ligand - mouse
3	176.5	10.5	261	2	S53090	CD40 ligand - bovi
4	175.5	10.4	278	2	A49266	fas ligand - rat
5	158.5	9.4	261	2	I53476	CD40 ligand - huma
6	141.5	8.4	235	1	QWMSN	tumor necrosis fac
7	141	8.4	234	1	A25451	tumor necrosis fac
8	137	8.1	234	1	JH0529	tumor necrosis fac
9	133	7.9	233	1	QWHUN	tumor necrosis fac
10	132.5	7.9	235	2	I54490	tumor necrosis fac
11	131.5	7.8	235	2	JU0029	tumor necrosis fac
12	130.5	7.7	306	2	I49139	lymphotoxin-beta -
13	130	7.7	233	1	S22052	tumor necrosis fac



14	128	7.6	234	1	JQ1344	tumor necrosis fac
15	126.5	7.5	233	1	S24642	tumor necrosis fac
16	126	7.5	232	1	S12606	tumor necrosis fac
17	125.5	7.4	185	2	S52715	tumor necrosis fac
18	122	7.2	193	2	S06192	tumor necrosis fac
19	120	7.1	260	2	S21738	CD40 ligand - mous
20	117	6.9	233	2	S11688	tumor necrosis fac
21	117	6.9	244	2	A46066	lymphotoxin beta -
22	97.5	5.8	1464	1	CGHU1S	collagen alpha 1(I
23	94.5	5.6	664	2	C84747	probable protein k
24	92.5	5.5	205	1	QWHUX	lymphotoxin alpha
25	92.5	5.5	450	2	S38114	hypothetical prote
26	91.5	5.4	3848	2	T17414	TipC protein - sli
27	91	5.4	493	2	AC0937	probable GntR-fami
28	90.5	5.4	1694	2	S50065	sialoadhesin - mou
29	90	5.3	730	2	JC1456	gelatinase B (EC 3
30	89.5	5.3	331	2	AF3526	homoproteocatechuat
31	89.5	5.3	379	2	A47659	farnesyl-protein t
32	89	5.3	202	1	B27303	tumor necrosis fac
33	89	5.3	440	2	I49681	glyceraldehyde-3-p
34	89	5.3	479	2	A25052	fibrinogen beta ch
35	89	5.3	639	2	C83624	probable two-compo
36	88.5	5.3	565	2	C89893	hypothetical prote
37	88.5	5.3	578	2	S51379	probable phosphoes
38	88.5	5.3	684	2	T01267	leucine-rich repea
39	88.5	5.3	883	2	A49733	[heparan sulfate]-
40	87.5	5.2	610	2	T06690	galactonolactone d
41	87.5	5.2	1466	1	CGHU7L	collagen alpha 1(I
42	87	5.2	639	2	A32935	protein P1 - Entam
43	87	5.2	1114	2	JH0284	125K surface antig
44	87	5.2	1315	2	G96722	hypothetical prote
45	86.5	5.1	279	2	F72339	hypothetical prote

#### ALIGNMENTS

##### RESULT 1

I38707

Fas ligand - human

C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 21-Jul-2000

C;Accession: I38707; JC2340; S57565; I38554

R;Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.

Int. Immunol. 6, 1567-1574, 1994

A;Title: Human Fas ligand: gene structure, chromosomal location and species specificity.

A;Reference number: I38707; MUID:95127560; PMID:7826947

A;Accession: I38707

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-281 <RES>

A;Cross-references: EMBL:U11821; NID:g595430; PIDN:AAC50124.1; PID:g595431

R;Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioaka, T.; Kasahara, A.; Fusamoto, H.; Kamada, T.

Biochem. Biophys. Res. Commun. 204, 468-474, 1994

A;Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.

A;Reference number: JC2340; MUID:95071350; PMID:7980502  
 A;Accession: JC2340  
 A;Molecule type: DNA  
 A;Residues: 1-281 <MIT>  
 A;Cross-references: GB:D38122; DDBJ:D29820; NID:g601892; PIDN:BAA07320.1; PID:g1369902  
 R;Schatzlein, C.E.  
 submitted to the EMBL Data Library, June 1995  
 A;Reference number: S57565  
 A;Accession: S57565  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-281 <SCH>  
 A;Cross-references: EMBL:X89102; NID:g887455; PID:g887456  
 R;Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; Goodwin, R.G.; Smith, C.A.; Ramsdell, F.; Lynch, D.H.  
 J. Exp. Med. 181, 71-77, 1995  
 A;Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.  
 A;Reference number: I38554; MUID:95105731; PMID:7528780  
 A;Accession: I38554  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-281 <RE2>  
 A;Cross-references: EMBL:U08137; NID:g624627; PIDN:AAC50071.1; PID:g624628  
 C;Genetics:  
 A;Gene: FasL  
 A;Introns: 151/1; 116/3  
 C;Keywords: glycoprotein; transmembrane protein  
 F;80-102/Domain: transmembrane #status predicted <TMM>  
 F;76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.2%; Score 189; DB 2; Length 281;  
 Best Local Similarity 21.7%; Pred. No. 1.9e-08;  
 Matches 69; Conservative 43; Mismatches 98; Indels 108; Gaps 11;

Qy	22	PGAPHEGPLHAPPPAP----	HQPPAASRS-----	MFVALLGLGLGQVVCS	63
				:	
Db	46	PPPPPPPLPPPPPPPLPPLPLPPLKKRGNHSTGLCLLMFFMVLVALVGLGLG-----			100
Qy	64	VALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAF			123
		:	: : :   :		
Db	101	--MFQLFHLQ-----	KELAELESTSQMHTA-----		124
Qy	124	QGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLT--	INATDIPSGSHK		181
		: : :   : :	:           : :		
Db	125	--SSLEKQIGH-----	PSPPEKKELRKVAHLTGKSNRSRSM-----		159
Qy	182	VSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLMVY			241
		:   : :     : :     : :     :			
Db	160	---LEWEDTYGIVLLSGVKYKGGGLVINETGLYFVYSKVYFRGQSCNN-----	LPLSHK		210
Qy	242	VTKTSIKIPSSHTLMKGGSTKY-----	WSGNSEHFYSINVG GFFKLRS GEEISIEVSN		295
		:     :   :     : :       : : :			
Db	211	VYMRNSKYPQDLVMEGKMMSYCTTGQMWARSS-----	YLGAVFNLT SADHLYVNVSE		263
Qy	296	PSLLDPDQDATYFGAFKV			313

||:: :: |::| ::|:  
Db 264 LSLVNFEEESQTFGLYKL 281

RESULT 2

A53062

Fas ligand - mouse

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999

C;Accession: A53062

R;Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nagata, S.

Cell 76, 969-976, 1994

A;Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in the Fas ligand.

A;Reference number: A53062; MUID:94185175; PMID:7511063

A;Accession: A53062

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-279 <TAK>

A;Cross-references: GB:U06948; NID:g473564; PIDN:AAA17800.1; PID:g473565

Query Match 10.9%; Score 184.5; DB 2; Length 279;  
Best Local Similarity 21.7%; Pred. No. 4.6e-08;  
Matches 70; Conservative 45; Mismatches 106; Indels 101; Gaps 11;

Qy 13 RGSEEMGGGPGAPHEGPLHAPPPAPHQP-----PAASRSMFVALLGLGL 57  
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Db 38 RGPDQRRPPPPPPVSPPLPPPSQPLPLPPLTPLKKKDHTNLWLPVVFFMVLVALVGMGL 97

Qy 58 GQVVCVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCR 117  
| :|:: |

Db 98 G-----MYQLFHL----- 105

Qy 118 RIKQAFQGA VQKELQHI--VGSQHRA---EKAMVDGSWLDLAKRSKLEAQPFAHLTINA 172  
||| : :| :: || : : | | : ||| |

Db 106 -----QKELAE LREFTNQSLKVSSF EKQIANPS----TPSEKKEPRSV AHLTGN- 150

Qy 173 TDIPSGSHKVSL S-SWYHDRGWAKISNM TFSNGKLIVNQDGFYYLYANICFRHHETSGDL 231  
| | : | | | | : : | |::| : | |::| : : | | : :

Db 151 -----PHSR SIPLEWEDTYGTALISGVKYKKGGLVINETGLYFVYSKVYFRGQSCN--- 201

Qy 232 ATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISI 291  
: | ||: : | | ||: | : : :| :| | | : : :

Db 202 -NQPLNHKVYMRNS--KYPEDLVLME EKRLNYCT-TGQIWAHSSYLGA VFNLT SADHLYV 257

Qy 292 EVSNPSLLDPDQDATYFGAFKV 313  
:| ||:: :: |::| ::|

Db 258 NISQLSLINFEE SKTFFGLYKL 279

RESULT 3

S53090

CD40 ligand - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 08-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 05-Nov-1999

C;Accession: S53090

R;Mertens, B.E.L.C.; Muriuki, M.  
submitted to the EMBL Data Library, February 1995  
A;Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.  
A;Reference number: S53090  
A;Accession: S53090  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-261 <MER>  
A;Cross-references: EMBL:Z48469; NID:g732569; PIDN:CAA88363.1; PID:g732570

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RESULT 4
A49266
fas ligand - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: A49266
R;Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.
Cell 75, 1169-1178, 1993
A;Title: Molecular cloning and expression of the Fas ligand, a novel member of
the tumor necrosis factor family.
A;Reference number: A49266; MUID:94084792; PMID:7505205
A;Accession: A49266
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-278 <SUD>
A;Cross-references: GB:U03470; NID:g440178; PIDN:AAC52129.1; PID:g440179
C;Keywords: glycoprotein; transmembrane protein

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Qy 21 GPGAPHEGPLHAPPPAPHPQPPAASRSM-----FVALLGLGL 57  
 ||| | |||:| |: : |||:|:|  
 Db 39 GPGQRRPPP--PPPPSPPLPPPSQPPPLPPLSPLKKKDNIELWLPVIFFMVLVALVGMGL 96

Qy 58 GQVVCVSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCR 117  
 | : | | : : | | : | : | : | : : :  
 Db 97 G-----MYQLFHLQKELAELEFTNHSI-RVSSFQKQIANPSTPSETKKPRSV----- 143

Qy 118 RIKQAFQGAQKELQHIVGSGHIRAEKAMVDGSWLDLAKRSKLEAQPFALHTINATDIPS 177  
 |||| |  
 Db 144 -----AHLTG NPR----- 151

Qy 178 GSHKVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQ 237  
 | : | | | | : : | | : : | | : : | | : : |  
 Db 152 -SRSIPL-EWEDTYGTALISGVKYKGGGLVINEAGLYFVYSKVYFRGQSCN----SQPLS 205

Qy 238 LMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFKLRSGEIEISIEVSNPS 297  
 ||: : | | ||: | : : : | : | | : : : | |  
 Db 206 HKVYM--RNFKYPGDLVLMEEKKLNCT-TGQIWAHSSYLGAVFNLTVADHLYVNISQLS 262

Qy 298 LLDPDQDATYFGAFKV 313  
 |:: : |::| :|:  
 Db 263 LINFEESKTFFGLYKL 278

# RESULT 5

I53476

CD40 ligand - human

N;Alternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein

C;Species: Homo sapiens (man)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 20-Apr-2001

C;Accession: S28017; JH0793; S26694; S28852; I53476; S25684; S30593

R;Hollenbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Braesch-Andersen, S.; Noelle, R.J.; Stamenkovic, I.; Ledbetter, J.A.; Aruffo, A. EMBO J. 11, 4313-4321, 1992

A;Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand for the CD40 receptor: expression of a soluble form of gp39 with B cell co-stimulatory activity.

A;Reference number: S28017; MUID:93049181; PMID:1385114

A;Accession: S28017

A;Molecule type: mRNA

A;Residues: 1-261 <HOL>

A;Cross-references: EMBL:Z15017; NID:g38483; PIDN:CAA78737.1; PID:g38484

R;Spriggs, M.K.; Armitage, R.J.; Strockbine, L.; Clifford, K.N.; Macduff, B.M.; Sato, T.A.; Maliszewski, C.R.; Fanslow, W.C. J. Exp. Med. 176, 1543-1550, 1992

A;Title: Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin E secretion.

A;Reference number: JH0793; MUID:93094757; PMID:1281209

A;Accession: JH0793

A;Molecule type: mRNA

A;Residues: 1-261 <SPR>

A;Cross-references: GB:X67878; NID:g38411; PIDN:CAA48077.1; PID:g38412

A;Experimental source: peripheral blood T-cell

R;Graf, D.; Korthaeuer, U.; Mages, H.W.; Senger, G.; Kroczeck, R.A.

Eur. J. Immunol. 22, 3191-3194, 1992

A;Title: Cloning of TRAP, a ligand for CD40 on human T cells.  
 A;Reference number: S26694; MUID:93076854; PMID:1280226  
 A;Accession: S26694  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-261 <GRA>  
 A;Cross-references: EMBL:X68550; NID:g37269; PIDN:CAA48554.1; PID:g37270  
 R;Gauchat, J.F.; Aubry, J.P.; Mazzei, G.; Life, P.; Jomotte, T.; Elson, G.;  
 Bonnefoy, J.Y.  
 FEBS Lett. 315, 259-266, 1993  
 A;Title: Human CD40-ligand: molecular cloning, cellular distribution and  
 regulation of expression by factors controlling IgE production.  
 A;Reference number: S28852; MUID:93138085; PMID:7678552  
 A;Accession: S28852  
 A;Molecule type: mRNA  
 A;Residues: 1-261 <GAU>  
 A;Cross-references: EMBL:L07414; NID:g180123; PIDN:AAA35662.1; PID:g180124  
 A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having  
 6-Gln  
 C;Genetics:  
 A;Gene: GDB:CD40LG; HIGM1; IMD3  
 A;Cross-references: GDB:120632; OMIM:308230  
 A;Map position: Xq26-Xq26  
 C;Keywords: glycoprotein; transmembrane protein  
 F;13-44/Domain: transmembrane #status predicted <TMM>  
 F;45-261/Domain: extracellular #status predicted <EXT>  
 F;6,240/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.4%; Score 158.5; DB 2; Length 261;  
 Best Local Similarity 24.5%; Pred. No. 6.8e-06;  
 Matches 68; Conservative 53; Mismatches 113; Indels 43; Gaps 15;

```

Qy      45 SRSMFVALLGLGL-GQVVCVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDT- 102
      |  :| : || : | |:: |      |  ::| :| ::      |||: | |
Db      20 SMKIFMYLLTVFLITQMIGSALFAVYLHRRLD--KIEDE-----RNLHEDFVFMKTI 69

Qy     103 -TLESQDTKLIPDSCRRIKQAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLE 161
      : : |  :| || |:: |  ::      : | :  : | : : | :
Db      70 QRCNTGERSLSLLNCEEIKSQFEGFV-KDIM-----LNKEETKKENSF-EMQKGDQ-N 119

Qy     162 AQPPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISN--MTFSNGK-LIVNQDGFYYLYA 218
      | ||: | :  |  | : |  ::| : ||  :| ||| | | : | ||: ||
Db     120 PQIAAHVISEAS-----SKTTSVLQW-AEKGYYTMSNNLVTLENGKQLTVKRQGLYYIYA 173

Qy     219 NICFRHHETSGDLATEYLQLMVYVTKTSIKIPS--SHTLMKGGSTKYWSGNSEFHFYSIN 276
      : | : : |  ::  :| |  |:: :| |  ||:
Db     174 QVTFCNREASSQAP-----FIASLCLKSPGRFERILLRAANTH--SSAKPCGQQSIH 224

Qy     277 VGGFFKLRSGEIEISIEVSNPSLLDPDQDATYFGAFKV 313
      :|| |:: |  : : |::|| :  | || | :
Db     225 LGGVFELQPGASVFVNVTDP SQVSHGTGFTSFGLLKL 261
  
```

RESULT 6  
 QWMSN  
 tumor necrosis factor alpha precursor - mouse  
 N;Alternate names: cachectin; TNF alpha

C;Species: Mus musculus (house mouse)  
 C;Date: 31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change 04-Feb-2000  
 C;Accession: A22908; S03791; A27303; A25164; A23127; A34251; I59058; A36696  
 R;Shirai, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.  
 DNA 7, 193-201, 1988  
 A;Title: Cloning and expression in Escherichia coli of the gene for mouse tumor necrosis factor.  
 A;Reference number: A22908; MUID:88224564; PMID:2836146  
 A;Accession: A22908  
 A;Molecule type: DNA  
 A;Residues: 1-235 <SHI>  
 A;Cross-references: GB:M20155  
 R;Shakhov, A.N.; Nedospasov, S.A.  
 Bioorg. Khim. 13, 701-705, 1987  
 A;Title: Molecular cloning of the genes coding for tumor necrosis factors: complete nucleotide sequence of the genomic copy of TNF-alpha in mice.  
 A;Reference number: S03791; MUID:87298639; PMID:3040015  
 A;Accession: S03791  
 A;Molecule type: DNA  
 A;Residues: 1-235 <SHA>  
 A;Cross-references: GB:M38296; NID:g202086; PIDN:AAA40459.1; PID:g202087  
 A;Note: article in Russian with English abstract  
 R;Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.  
 Nucleic Acids Res. 15, 9083-9084, 1987  
 A;Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha- (tumor necrosis factor) and TNF-beta-(lymphotoxin) genes.  
 A;Reference number: A93679; MUID:88067722; PMID:3684584  
 A;Accession: A27303  
 A;Molecule type: DNA  
 A;Residues: 1-235 <SEM>  
 A;Cross-references: GB:Y00467; NID:g54830; PIDN:CAA68530.1; PID:g54832  
 R;Pennica, D.; Hayflick, J.S.; Bringman, T.S.; Palladino, M.A.; Goeddel, D.V.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 6060-6064, 1985  
 A;Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor necrosis factor.  
 A;Reference number: A25164; MUID:85298296; PMID:3898078  
 A;Accession: A25164  
 A;Molecule type: mRNA  
 A;Residues: 1-235 <PEN>  
 A;Cross-references: GB:M11731; NID:g202084; PIDN:AAA40458.1; PID:g202085  
 R;Fransen, L.; Muller, R.; Marmenout, A.; Tavernier, J.; van der Heyden, J.; Kawashima, E.; Chollet, A.; Tizard, R.; van Heuverswyn, H.; van Vliet, A.; Ruysschaert, M.R.; Fiers, W.  
 Nucleic Acids Res. 13, 4417-4429, 1985  
 A;Title: Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic expression.  
 A;Reference number: A23127; MUID:85242112; PMID:2989794  
 A;Accession: A23127  
 A;Molecule type: mRNA  
 A;Residues: 1-235 <FRA>  
 A;Cross-references: GB:X02611; NID:g54844; PIDN:CAA26457.1; PID:g54845  
 R;Cseh, K.; Beutler, B.  
 J. Biol. Chem. 264, 16256-16260, 1989  
 A;Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide results in a larger, inactive form of secreted protein.  
 A;Reference number: A34251; MUID:89380231; PMID:2777790  
 A;Accession: A34251

A;Molecule type: protein  
A;Residues: 70-87 <CSE>  
R;Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A.  
Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986  
A;Title: Identification of a common nucleotide sequence in the 3'-untranslated  
region of mRNA molecules specifying inflammatory mediators.  
A;Reference number: I59058; MUID:86149365; PMID:2419912  
A;Accession: I59058  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-230,'R',232-235 <RES>  
A;Cross-references: GB:M13049; NID:g202082; PIDN:AAA40457.1; PID:g202083  
R;Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.  
Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990  
A;Title: Characterization of high molecular weight glycosylated forms of murine  
tumor necrosis factor.  
A;Reference number: A36696; MUID:91097531; PMID:2268312  
A;Accession: A36696  
A;Molecule type: protein  
A;Residues: 80-85,'X',87-99 <SHE>  
C;Genetics:  
A;Introns: 62/3; 81/1; 97/1  
A;Note: the first intron occurs in the 5'-untranslated region  
C;Superfamily: tumor necrosis factor  
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine;  
macrophage; membrane protein; myristylation  
F;80-235/Product: tumor necrosis factor #status experimental <MAT>  
F;20/Binding site: myristate (Lys) (covalent) #status predicted  
F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted  
F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;148-179/Disulfide bonds: #status predicted

Query Match 8.4%; Score 141.5; DB 1; Length 235;  
Best Local Similarity 25.9%; Pred. No. 0.00017;  
Matches 42; Conservative 28; Mismatches 57; Indels 35; Gaps 7;

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Qy      163 QPFAHLTINATDIPSGSHKVSLS-SWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANI 220
          :| ||: | | :| | | :| | : :|:| || | :|: :
Db      90 KPAHVVAN-----HQVEEQLEWLSQRANALLANGMDLKDNLVVPADGLYLVYSQV 141

Qy      221 CFRHHETSGDLATEYLQLMVYVTK-----TSIKIPSSHTLMKGGSTKYWSGNS 268
          |: | :|: | | :| : :| | :| | |
Db      142 LEK-----GQGCPDYVLLTHTVSRFAISYQEKVNLLSAVKSPCPKDTPEGAELKPW---- 192

Qy      269 EFHFYSINVGGFFKLRSGEESIEVSNPSLLD-PDQDATYFG 309
          : | :|| |:| |::| ||: | || : |||
Db      193 ---YEPIYLGGVFQLEKGDQLSAEVNLPKYLDFAESGQVYFG 231

```

# RESULT 7

A25451

tumor necrosis factor alpha precursor - rabbit

N;Alternate names: cachectin; TNF alpha

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000

C;Accession: A25454; A25451; JS0727



R;Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi, H.; Kato, M.; Seko, M.  
DNA 5, 149-156, 1986  
A;Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for rabbit tumor necrosis factor.  
A;Reference number: A25454; MUID:86219711; PMID:3519137  
A;Accession: A25454  
A;Molecule type: mRNA  
A;Residues: 1-234 <ITO>  
A;Cross-references: GB:M12845; NID:g165759; PIDN:AAA31486.1; PID:g165760  
R;Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.  
DNA 5, 157-165, 1986  
A;Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.  
A;Reference number: A25451; MUID:86219712; PMID:3519138  
A;Accession: A25451  
A;Molecule type: DNA  
A;Residues: 1-234 <IT2>  
A;Note: this sequence differs from that shown in having a Gln inserted between residues 62 and 63  
R;Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.  
Gene 95, 215-221, 1990  
A;Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF-beta (lymphotoxin) and TNF-alpha (tumor necrosis factor).  
A;Reference number: JH0309; MUID:91065534; PMID:2249779  
A;Accession: JS0727  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-62,'Q',63-234 <SHA>  
A;Cross-references: GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31484.1; PID:g165756  
C;Genetics:  
A;Introns: 62/3; 80/1; 96/1  
C;Superfamily: tumor necrosis factor  
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membrane protein; myristylation  
F;1-81/Domain: propeptide #status predicted <PRO>  
F;82-234/Product: tumor necrosis factor #status predicted <MAT>  
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted  
F;83/Binding site: carbohydrate (Ser) (covalent) #status predicted  
F;147-178/Disulfide bonds: #status predicted

Query Match 8.4%; Score 141; DB 1; Length 234;  
Best Local Similarity 21.6%; Pred. No. 0.00018;  
Matches 65; Conservative 35; Mismatches 99; Indels 102; Gaps 13;

Qy	27	EGPLHAPPPPAPHQPPAASR----	SMFVALLGLGLGQVVCSVALFFYFRAQMDPNRISED	82
			:   :	:
Db	14	EGPL----PKKAGGPQGSKRCLCLSLFSFLLVAGATTLCF----	LLHFRVIGPQEEESPN	65
Qy	83	GTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGA	VQKELQHIVGSQHIRA	142
		:		
Db	66	NLHLV-----NPVAQMVTLSR-----	A	82
Qy	143	EKAMVDGSWLIDLAKRSKLEAQPF	FAHLTINATDIPSGSHKVSLS	SSWYHDRGWAKISN-MTF
		:   :	:       :	:         :
Db	83	SRALSD-----	KPLAHVVAN----	PQVEGQL---QWLSQRANALLANGMKL
				121

Qy 202 SNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKG--- 258  
 :: :|:| || | :|: : | || | : | | : : : | : | :  
 Db 122 TDNQLVVPADGLYLIYSQVLF-----SGQGCRSYVLLTHTVSRFAVSYPNKNVLLSAIKS 176

Qy 259 -----GSTKYWSGNSEFHFYSINVGGFFKLRSGEESISIEVSNPSLLD-PDQDATYF 308  
 | : | :|| |:| | : :| ||: | || : ||  
 Db 177 PCHRETPEEAEPMAW-----YEPIYLGGVFQLEKGDRLSTEVNQPEYLDLAESGQVYF 229

Qy 309 G 309  
 |  
 Db 230 G 230

# RESULT 8

JH0529

tumor necrosis factor alpha precursor - sheep

N;Alternate names: cachectin; TNF alpha

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000

C;Accession: JH0529; S48118; S13114; S20661

R;Green, I.R.; Sargan, D.R.

Gene 109, 203-210, 1991

A;Title: Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems with cloning by inverse PCR.

A;Reference number: JH0529; MUID:92112044; PMID:1765267

A;Accession: JH0529

A;Molecule type: mRNA

A;Residues: 1-234 <GRE>

A;Cross-references: EMBL:X55152; NID:g1405; PIDN:CAA38952.1; PID:g1406

A;Experimental source: alveolar macrophage

R;Nash, A.D.; Barcham, G.J.; Brandon, M.R.; Andrews, A.E.

Immunol. Cell Biol. 69, 273-283, 1991

A;Title: Molecular cloning, expression and characterization of ovine TNF-alpha.

A;Reference number: S48118; MUID:92155784; PMID:1786996

A;Accession: S48118

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-234 <NAS>

A;Cross-references: EMBL:X56756; NID:g297806; PIDN:CAA40076.1; PID:g297807

R;Young, A.J.; Hay, J.B.; Chan, J.Y.C.

Nucleic Acids Res. 18, 6723, 1990

A;Title: Primary structure of ovine tumor necrosis factor alpha cDNA.

A;Reference number: S13114; MUID:91067496; PMID:2251151

A;Accession: S13114

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-62,64-234 <YOU>

A;Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g1404

A;Note: comparison with the introns of homologous sequences suggest that this is probably an alternative splicing

C;Superfamily: tumor necrosis factor

C;Keywords: alternative splicing; cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; myristylation; transmembrane protein

F;1-77/Domain: propeptide #status predicted <PRO>

F;78-234/Product: tumor necrosis factor alpha #status predicted <TUM>

F;20/Binding site: myristate (Lys) (covalent) #status predicted

```
F;82/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;96/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;146-178/Disulfide bonds: #status predicted
```

Qy	134	IVGSQHIRAEKAMVDGSW---LDLAKRSKLEA---QPF AHLTINATDIPSGSHKVSLSW	187
		::      ::   :     :     :	
Db	55	VIGPQ--REEQSPAGPSFNRPLVQTLRSSSQASNNKPVAHVVAN-----ISAP	100
Qy	188	YHDRGWAKISNMTFNSG-----KLIVNQDGFYYLYANICFRHH-----ETSGDL	231
		:  :   : :       : : :        :	
Db	101	GQLRWGDSYANALMANGVELKDNQLVVPTDGLYLIYSQVLFRGHGCPSTPLFLTHTISRI	160
Qy	232	ATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGF FKLRS GEEISI	291
		: :     :      :       :    : :	
Db	161	AVSY-QTKVNIL-SAIKSPCHRETLEGAEAKPW-----YEPIYQGGVFQLEKGDRLSA	211
Qy	292	EVSNPSSL D-PDQDATYFG	309
		::      :	
Db	212	EINLPEYLDYAESGOVYFG	230

R;Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.; Kohr, W.J.; Aggarwal, B.B.; Goeddel, D.V.  
Nature 312, 724-729, 1984

A;Title: Human tumour necrosis factor: precursor structure, expression and homology to lymphotoxin.  
A;Reference number: A93351; MUID:85086244; PMID:6392892  
A;Accession: A93351  
A;Molecule type: mRNA  
A;Residues: 1-233 <PEN>  
A;Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210  
A;Note: this protein was isolated from the monocyte-like cell line HL-60 from a promyelocytic leukemia

R;Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdell, J.N.; Yamamoto, R.; Mark, D.F.  
Science 228, 149-154, 1985

A;Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.  
A;Reference number: A44189; MUID:85142190; PMID:3856324  
A;Accession: A44189  
A;Molecule type: mRNA  
A;Residues: 1-62,'S',64-233 <WAN>  
A;Cross-references: GB:M10988; NID:g339737; PIDN:AAA61198.1; PID:g339738

R;Fukuda, S.; Ando, S.; Sanou, O.; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; Ando, O.; Torigoe, K.; Sugimoto, T.; Kurimoto, M.  
Lymphokine Res. 7, 175-185, 1988

A;Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and interferon-alpha from BALL-1 cells stimulated by HVJ.  
A;Reference number: A61478; MUID:88301617; PMID:2841543  
A;Accession: B61478  
A;Molecule type: protein  
A;Residues: 83-102;109-119;121-128,'X',130-131;142-144,'X',146,'XXX',150-152;159-174;180,'X',182-204 <FUK>

R;Marmenout, A.; Franssen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima, E.; Shaw, A.; Johnson, M.  
Eur. J. Biochem. 152, 515-522, 1985

A;Title: Molecular cloning and expression of human tumor necrosis factor and comparison with mouse tumor necrosis factor.  
A;Reference number: I53311; MUID:86030296; PMID:3932069  
A;Accession: I53311  
A;Status: translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-233 <MAR>  
A;Cross-references: GB:M26331; NID:g339763; PIDN:AAA36758.1; PID:g339764  
A;Experimental source: U-937 cells

R;Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.  
Eur. J. Biochem. 235, 431-437, 1996

A;Title: O-Glycosylated species of natural human tumor-necrosis factor-alpha.  
A;Reference number: S62610; MUID:96202967; PMID:8631363  
A;Accession: S62610  
A;Molecule type: protein  
A;Residues: 77-99 <TAK>

R;D'Alfonso, S.; Richiardi, P.M.  
Immunogenetics 39, 150-154, 1994

A;Title: A polymorphic variation in a putative regulation box of the TNFA promoter region.  
A;Reference number: I54522; MUID:94102809; PMID:7903959

A;Accession: I54522  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-8 <DAL>  
 A;Cross-references: GB:S68530; NID:g544751  
 R;Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.  
 J. Exp. Med. 176, 1053-1062, 1992  
 A;Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific lysine residues.  
 A;Reference number: A59163; MUID:93018820; PMID:1402651  
 A;Contents: annotation; identification of myristylated lysines  
 R;Aggarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Bringman, T.S.; Nedwin, G.E.; Goeddel, D.V.; Harkins, R.N.  
 J. Biol. Chem. 260, 2345-2354, 1985  
 A;Title: Human tumor necrosis factor. Production, purification, and characterization.  
 A;Reference number: A92511; MUID:85130974; PMID:3871770  
 A;Contents: annotation; disulfide bond  
 C;Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induction, TNF-alpha can cause cytolysis of certain tumor cell lines and have an antiproliferative effect on others without detriment to normal cells. It can also act synergistically with interferon gamma to kill certain transformed cell lines.  
 C;Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes closely linked on chromosome 6. They are induced by similar mitogenic stimuli and have similar biological activities but are produced by different cell types and have different induction kinetics.  
 C;Genetics:  
 A;Gene: GDB:TNF; TNFA  
 A;Cross-references: GDB:120441; OMIM:191160  
 A;Map position: 6p21.3-6p21.3  
 A;Introns: 62/3; 78/1; 94/1  
 C;Complex: homotrimer  
 C;Superfamily: tumor necrosis factor  
 C;Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; macrophage; membrane protein; myristylation  
 F;1-76/Domain: propeptide #status predicted <PRO>  
 F;77-233/Product: tumor necrosis factor #status experimental <MAT>  
 F;19,20/Binding site: myristate (Lys) (covalent) #status experimental  
 F;81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental  
 F;145-177/Disulfide bonds: #status experimental

Query Match 7.9%; Score 133; DB 1; Length 233;  
 Best Local Similarity 25.5%; Pred. No. 0.00086;  
 Matches 40; Conservative 31; Mismatches 62; Indels 24; Gaps 8;

```

Qy      163 QPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANIC 221
      :| ||: |   |   ::   | : | | ::| :   : ||: | | :| :
Db      87 KPAHVVAN----PQAEQQL---QWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVL 139

Qy      222 FRHH--ETSGDLATEYLQLMV--YVTK----TSIKIPSSHTLMKGGSTKYWSGNSEFHFY 273
      |:   :: | | : : | ||   :|| |   :| | |   :
Db      140 FKGQGPCSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPW-----YE 192

Qy      274 SINVGGFVKLRSGEEISIEVSNPSLLD-PDQDATYFG 309
      | :|| ||: | : :| |:: | || :   |||
Db      193 PIYLGGVFQLEKGDRLSAEINRPDYLDFAESGQVYFG 229
  
```

RESULT 10

I54490

tumor necrosis factor alpha precursor - white-footed mouse

C;Species: Peromyscus leucopus (white-footed mouse)

C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 04-Feb-2000

C;Accession: I54490

R;Crew, M.D.; Filipowsky, M.E.

Immunogenetics 35, 351-353, 1992

A;Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leucopus (family Cricetidae).

A;Reference number: I54490; MUID:92218012; PMID:1348497

A;Accession: I54490

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-235 <RES>

A;Cross-references: GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507

C;Genetics:

A;Gene: PlTNF

A;Introns: 62/3; 81/1; 97/1

C;Superfamily: tumor necrosis factor

C;Keywords: glycoprotein; lipoprotein; myristylation

F;19,20/Binding site: myristate (Lys) (covalent) #status predicted

F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 7.9%; Score 132.5; DB 2; Length 235;

Best Local Similarity 25.3%; Pred. No. 0.00096;

Matches 42; Conservative 27; Mismatches 54; Indels 43; Gaps 7;

Qy 163 QPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISNMTFSG-----KLIVNQDGFYYL 216

:| ||: | :| : || :|| :|| :|| :|| :| :

Db 90 KPAHVVAN-----HQVDEQLEWLSRG----ANALLANGMDLKDNLVIPADGLYLV 137

Qy 217 YANICFRHHETSGDLATEYLQLMVYVTK-----TSIKIPSSHTLMKGGSTKYW 264

|: : |: | : |: | |: : :|| | :| | |

Db 138 YSQVLEK-----GQGCSSYVLLTHTVSRFAVSIEDKVNLLSAIKSPCPKETPEGSELKPW 192

Qy 265 SGNSEFHFYSINVGGFFKLRSGEIEISIEVSNPSLLD-PDQDATYFG 309

: | :|| |:| |: :| ||: | || : |||

Db 193 -----YEPIYLGGVFQLEKGDRLSAEVNLPKYLDFAESGQVYFG 231

RESULT 11

JU0029

tumor necrosis factor alpha precursor - rat

N;Alternate names: cachectin; TNF alpha

C;Species: Rattus norvegicus (Norway rat)

C;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 04-Feb-2000

C;Accession: JU0029; JN0868; S21674

R;Shirai, T.; Shimizu, N.; Horiguchi, S.; Ito, H.

Agric. Biol. Chem. 53, 1733-1736, 1989

A;Title: Cloning and expression in Escherichia coli of the gene for rat tumor necrosis factor.

A;Reference number: JU0029

A;Accession: JU0029

A;Molecule type: DNA

A;Residues: 1-235 <SHI>  
R;Kwon, J.; Chung, I.Y.; Benveniste, E.N.  
Gene 132, 227-236, 1993  
A;Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.  
A;Reference number: JN0868; MUID:94040766; PMID:8224868  
A;Accession: JN0868  
A;Molecule type: DNA  
A;Residues: 1-235 <KWO>  
A;Cross-references: GB:L00981; NID:g205253; PIDN:AAA16275.1; PID:g205254  
R;Estler, H.C.; Grewe, M.; Gaussling, R.; Pavlovic, M.; Decker, K.  
Biol. Chem. Hoppe-Seyler 373, 271-281, 1992  
A;Title: Rat tumor necrosis factor-alpha. Transcription in rat Kupffer cells and in vitro posttranslational processing based on a PCR-derived cDNA.  
A;Reference number: S21674; MUID:92329007; PMID:1627266  
A;Accession: S21674  
A;Molecule type: mRNA  
A;Residues: 1-38,'P',40-162,'T',164-201,'S',203-235 <EST>  
A;Cross-references: GB:X66539; GB:S40199; NID:g395369; PIDN:CAA47146.1; PID:g395370  
C;Comment: Tumor necrosis factor is secreted by macrophages in response to endotoxin and produces hemorrhagic necrosis of tumors.  
C;Genetics:  
A;Gene: TNF-alpha  
A;Introns: 62/3; 81/1; 97/1  
C;Superfamily: tumor necrosis factor  
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membrane protein; myristylation  
F;80-235/Product: tumor necrosis factor #status predicted <MAT>  
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted  
F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted  
F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;148-179/Disulfide bonds: #status predicted

Query Match 7.8%; Score 131.5; DB 2; Length 235;  
Best Local Similarity 25.3%; Pred. No. 0.0012;  
Matches 41; Conservative 27; Mismatches 59; Indels 35; Gaps 7;

```

Qy      163 QPFAHLTINATDIPSGSHKVSLS-SWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANI 220
          :| ||: |           |:           | | :|| | : :|| | || | :|: :
Db      90 KPAHVVAN-----HQAEQLEWLSQRANALLANGMDLKDNLVVPADGLYLIYSQV 141

Qy      221 CFRHHETSGDLATEYLQLMVYVTK-----TSIKIPSSHTLMKGGSTKYWSGNS 268
          |:           | :|: | |:           :|| | :| | |
Db      142 LFK-----GQGCPDYVLLTHTVSRFAISYQEKVSLLSAIKSPCKDTPEGAELKPW---- 192

Qy      269 EFHFYISINVGGFFKLRSGEEISIEVSNPSLLD-PDQDATYFG 309
          : : :|| |:| |: :| ||: | || :   |||
Db      193 ---YEPMYLGGVFQLEKGDLLSAEVNLPKYLDITESGQVYFG 231

```

# RESULT 12

I49139

lymphotoxin-beta - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999

C;Accession: I49139; I49138; I49076

R;Lawton, P.; Nelson, J.; Tizard, R.; Browning, J.L.  
 J. Immunol. 154, 239-246, 1995  
 A;Title: Characterization of the mouse lymphotoxin-beta gene.  
 A;Reference number: I49138; MUID:95088371; PMID:7995944  
 A;Accession: I49139  
 A;Status: translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-306 <RES>  
 A;Cross-references: EMBL:U16985; NID:g577830; PIDN:AAA70089.1; PID:g577831  
 A;Accession: I49138  
 A;Status: translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-306 <RE3>  
 A;Cross-references: EMBL:U16984; NID:g577431; PIDN:AAB60493.1; PID:g577432  
 R;Pokholok, D.K.; Maroulakou, I.G.; Kuprash, D.V.; Alimzhanov, M.B.; Kozlov, S.V.; Novobrantseva, T.I.; Turetskaya, R.L.; Green, J.E.; Nedospasov, S.A.  
 Proc. Natl. Acad. Sci. U.S.A. 92, 674-678, 1995  
 A;Title: Cloning and expression analysis of the murine lymphotoxin beta gene.  
 A;Reference number: A55602; MUID:95148600; PMID:7846035  
 A;Accession: I49076  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-306 <RE2>  
 A;Cross-references: EMBL:U12029; NID:g515508; PIDN:AAA67716.1; PID:g515509  
 C;Genetics:  
 A;Gene: LT-beta  
 A;Introns: 54/3; 160/1

Query Match 7.7%; Score 130.5; DB 2; Length 306;  
 Best Local Similarity 22.1%; Pred. No. 0.002;  
 Matches 55; Conservative 38; Mismatches 87; Indels 69; Gaps 12;

```

Qy      105 ESQDTKLIP---DSCRRIKQAFQGA VQKELQHIVGSQHIRAEKAMVDG SWLDLAKRSKLE 161
          | : | : | | : : | : | | | | | | | | | | | | | | | | | | | | | |
Db      86 ETPDPR LHPQRSNASRNLASTSQGPV-----AQSSREASAWMTI----- 124

Qy      162 AQPFAHLTIN--ATDIPSGSHKVSLS-----SWYHDRG--WAKISNMTF----- 201
          | | | | : : | | : | : | | | | | | | | | | | | | | | | | | |
Db      125 LSPAADSTPDPGVQQLPKGEPETDLNP ELPA AHLIGAWMSGQGLSWEASQEEAFLRSGAQ 184

Qy      202 ---SNGKLIVNQDGFYYLYANICFR-HHETSGDLATEYLQL--MVYVTKTSIKIPSSHTL 255
          : : | | : | | | | | | | : : | | : | | | | | | | | | | | | | |
Db      185 FSPTHG-LALPQDGVYYLYCHVGYRGRTPPAGRSRARS LTLRSALYRAGGAYGRGSPELL 243

Qy      256 MKGGST-----KYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLDPDQD 304
          : : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      244 LEGAETVTPVVDPIGYGSLW-----YTSVGF GGLAQLRSGERVYVNISHPDMVDYRRG 296

Qy      305 ATYFGAFKV 313
          | : | | | |
Db      297 KTFFGAVMV 305
```

RESULT 13  
 S22052  
 tumor necrosis factor alpha precursor - baboon  
 C;Species: Papio sp. (baboon)



C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000  
 C;Accession: S22052  
 R;Sanjanwala, M.; Edwards, A.  
 submitted to the EMBL Data Library, September 1991  
 A;Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.  
 A;Reference number: S22052  
 A;Accession: S22052  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-233 <SAN>  
 A;Cross-references: EMBL:X62141; NID:g38159; PIDN:CAA44068.1; PID:g38160  
 C;Genetics:  
 A;Introns: 62/3; 78/1; 94/1  
 C;Superfamily: tumor necrosis factor  
 C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein  
 F;19,20/Binding site: myristate (Lys) (covalent) #status predicted  
 F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted  
 F;145-177/Disulfide bonds: #status predicted

Query Match 7.7%; Score 130; DB 1; Length 233;  
 Best Local Similarity 25.5%; Pred. No. 0.0015;  
 Matches 40; Conservative 31; Mismatches 62; Indels 24; Gaps 8;

```

Qy      163 QPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANIC 221
          :| ||: |   |   ::   | : | | :| :   : :|:| :| | :|: :
Db      87 KPAHVVAN----PQAEQQL---QWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVL 139

Qy      222 FRHH--ETSGDLATEYLQLMV--YVTK----TSIKIPSSHTLMKGGSTKYWSGNSEFHFY 273
          |:   :: | | :   :   | ||   :|| |   :| | |   :
Db      140 FKGQGPCSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPW-----YE 192

Qy      274 SINVGGFKLRSGEEISIEVSNPSLLD-PDQDATYFG 309
          | :|| |:| |: :| |: : | || :   |||
Db      193 PIYLGGVFQLEKGDRLSAEINLPDYLDFAESGQVYFG 229

```

#### RESULT 14

JQ1344

tumor necrosis factor alpha precursor - horse

N;Alternate names: cachectin; TNF alpha

C;Species: Equus caballus (domestic horse)

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000

C;Accession: JQ1344

R;Su, X.; Morris, D.D.; McGraw, R.A.

Gene 107, 319-321, 1991

A;Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis factor alpha.

A;Reference number: JQ1344; MUID:92084125; PMID:1748301

A;Accession: JQ1344

A;Molecule type: DNA

A;Residues: 1-234 <SUX>

A;Cross-references: GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245

C;Comment: This protein is an important proximal mediator of endotoxemia.

C;Genetics:

A;Gene: TNF-alpha

A;Introns: 62/3; 79/1; 95/1

C;Superfamily: tumor necrosis factor  
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine;  
macrophage; membrane protein; myristylation  
F;78-234/Product: tumor necrosis factor alpha #status predicted <TUM>  
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted  
F;82/Binding site: carbohydrate (Ser) (covalent) #status predicted  
F;146-178/Disulfide bonds: #status predicted

Query Match 7.6%; Score 128; DB 1; Length 234;  
Best Local Similarity 24.2%; Pred. No. 0.0023;  
Matches 39; Conservative 32; Mismatches 58; Indels 32; Gaps 8;

```
Qy      163 QPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANIC 221
          :| ||: | | : : | | : : | : | | : | :
Db      88 KPVAVHVAN----PQAEQQL---QWLSGRANALLANGVKLTDNQLVVPDGLYLIYSQVL 140

Qy      222 FRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKG-----GSTKYWSGNSE 269
          |: | :| | | : : : | | | : | |
Db      141 FK---GQGCPSTHVL-LTHTISRLAVSYPSKVNLLSAIKSPCHTESPEQAEAKPW----- 191

Qy      270 FHFYSINVGGFKKLRSGEEISIEVSNPSLLD-PDQDATYFG 309
          : | :|| |:| |::| |:: |: || : |||
Db      192 --YEPIYLGGVFQLEKGDQLSAEINQPNYLDFAESGQVYFG 230
```

#### RESULT 15

S24642

tumor necrosis factor alpha precursor - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000

C;Accession: I46047; S24642

R;Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.

Cytokine 5, 336-341, 1993

A;Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and tumour necrosis factor-alpha genes.

A;Reference number: I46046; MUID:94083525; PMID:8260599

A;Accession: I46047

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-233 <CL2>

A;Cross-references: EMBL:Z14137; NID:g796; PIDN:CAA78511.1; PID:g798

C;Genetics:

A;Gene: TNFA

A;Introns: 62/3; 78/1; 94/1

C;Superfamily: tumor necrosis factor

C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

F;20/Binding site: myristate (Lys) (covalent) #status predicted

F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F;145-177/Disulfide bonds: #status predicted

Query Match 7.5%; Score 126.5; DB 1; Length 233;  
Best Local Similarity 25.5%; Pred. No. 0.0031;  
Matches 50; Conservative 25; Mismatches 80; Indels 41; Gaps 9;

```
Qy      134 IVGSQHIRAEKAMVDGSWDLAKRSKLEA---QPFAHLTINATDIPSGSHKVSLSWYHD 190
          :|| | : | | || :| :| ||: || |
Db      55 VIGPQREESPGGPSINSPLVQTLRSSSQASSNKPVAHV---VADINSPGQL----- 102
```

Qy	191	RGWAKISNMTFSNG-----KLIVNQDGFYLYANICFRHH-----ETSGDLATE	234
		:  :   :       :  :	
Db	103	RWWDSYANALMANGVKLEDNQLVVPADGLYLIYSQVLFQGGCPSTPLFLTHTISRIAVS	162
Qy	235	YLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESIEVS	294
		: :     :     :       :     :     :	
Db	163	Y-QTKVNIL-SAIKSPCHRETPEWAEAKPW-----YEPIYQGGVFQLEKGDRLSAEIN	213
Qy	295	NPSLLD-PDQDATYFG	309
		:	
Db	214	LPDYLDYAESGQVYFG	229

Search completed: September 15, 2004, 08:33:42  
Job time : 42 secs

OM protein - protein search, using sw model

Run on: September 15, 2004, 08:34:26 ; Search time 671 Seconds  
(without alignments)  
151.503 Million cell updates/sec

Title: US-09-211-315-39  
Perfect score: 1685  
Sequence: 1 MRRASRDYTKYLRGSEEMGG.....LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1335176 seqs, 320689617 residues

Total number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
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8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
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10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*  
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12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	%	Query					
No.	Score	Match Length	DB	ID			Description

1	1685	100.0	317	9	US-09-813-329-7	Sequence 7, Appli
2	1685	100.0	317	9	US-09-871-856-13	Sequence 13, Appl
3	1685	100.0	317	9	US-09-877-650-13	Sequence 13, Appl
4	1685	100.0	317	12	US-10-289-456-79	Sequence 79, Appl
5	1685	100.0	317	12	US-10-202-062-22	Sequence 22, Appl
6	1685	100.0	317	12	US-09-865-363-13	Sequence 13, Appl
7	1685	100.0	317	12	US-10-151-071-10	Sequence 10, Appl
8	1685	100.0	317	12	US-09-957-944-6	Sequence 6, Appli
9	1685	100.0	317	14	US-10-218-547-22	Sequence 22, Appl
10	1685	100.0	317	14	US-10-405-878-13	Sequence 13, Appl
11	1685	100.0	317	14	US-10-167-182-11	Sequence 11, Appl
12	1685	100.0	317	14	US-10-310-793-28	Sequence 28, Appl
13	1685	100.0	317	15	US-10-460-623-11	Sequence 11, Appl
14	1685	100.0	317	16	US-10-664-801-2	Sequence 2, Appli
15	1685	100.0	317	16	US-10-381-160-6	Sequence 6, Appli
16	1424.5	84.5	316	12	US-09-957-944-8	Sequence 8, Appli
17	1422	84.4	270	12	US-10-289-456-80	Sequence 80, Appl
18	1417.5	84.1	316	10	US-09-079-569-7	Sequence 7, Appli
19	1417.5	84.1	316	10	US-09-873-829-4	Sequence 4, Appli
20	1417.5	84.1	316	13	US-10-017-910-4	Sequence 4, Appli
21	1417.5	84.1	316	14	US-10-105-057-2	Sequence 2, Appli
22	1417.5	84.1	316	14	US-10-272-411-19	Sequence 19, Appl
23	1417.5	84.1	316	14	US-10-272-328A-19	Sequence 19, Appl
24	1417.5	84.1	316	14	US-10-326-052-2	Sequence 2, Appli
25	1417.5	84.1	316	14	US-10-167-182-1	Sequence 1, Appli
26	1417.5	84.1	316	15	US-10-460-623-1	Sequence 1, Appli
27	1417.5	84.1	316	16	US-10-664-801-4	Sequence 4, Appli
28	1417.5	84.1	316	16	US-10-664-801-6	Sequence 6, Appli
29	1326.5	78.7	294	9	US-09-871-856-11	Sequence 11, Appl
30	1326.5	78.7	294	9	US-09-877-650-11	Sequence 11, Appl
31	1326.5	78.7	294	12	US-09-865-363-11	Sequence 11, Appl
32	1326.5	78.7	294	14	US-10-405-878-11	Sequence 11, Appl
33	1325	78.6	250	15	US-10-338-785A-1	Sequence 1, Appli
34	1325	78.6	250	16	US-10-611-363-1	Sequence 1, Appli
35	1319	78.3	249	12	US-10-289-456-82	Sequence 82, Appl
36	1319	78.3	249	14	US-10-050-902-221	Sequence 221, App
37	1319	78.3	249	14	US-10-050-898-221	Sequence 221, App
38	1301	77.2	246	14	US-10-167-182-17	Sequence 17, Appl
39	1301	77.2	246	15	US-10-460-623-17	Sequence 17, Appl
40	1293	76.7	245	10	US-09-873-829-2	Sequence 2, Appli
41	1293	76.7	245	13	US-10-017-910-2	Sequence 2, Appli
42	1292	76.7	244	12	US-10-289-456-81	Sequence 81, Appl
43	1292	76.7	244	12	US-10-211-858-42	Sequence 42, Appl
44	1292	76.7	244	14	US-10-210-951-42	Sequence 42, Appl
45	1292	76.7	244	14	US-10-050-902-222	Sequence 222, App

#### ALIGNMENTS

RESULT 1  
 US-09-813-329-7  
 ; Sequence 7, Application US/09813329  
 ; Patent No. US20020012968A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bristol-Myers Suibb Company

```
; TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor
Class Molecule ("DmTNF") and
; TITLE OF INVENTION: Variants Thereof
; FILE REFERENCE: D0016.np
; CURRENT APPLICATION NUMBER: US/09/813,329
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,816
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-813-329-7
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Query Match          100.0%; Score 1685; DB 9; Length 317;
Best Local Similarity 100.0%; Pred. No. 1.2e-155;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
          |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy      61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
          |||
Db      61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy      121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHLTINATDIPSGSH 180
          |||
Db      121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHLTINATDIPSGSH 180

Qy      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYQLQMLV 240
          |||
Db      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYQLQMLV 240

Qy      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
          |||
Db      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy      301 PDQDATYFGAFKVRDID 317
          |||
Db      301 PDQDATYFGAFKVRDID 317
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# RESULT 2

US-09-871-856-13

; Sequence 13, Application US/09871856

; Patent No. US20020081720A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

```

;          STREET: 51 University Street
;          CITY: Seattle
;          STATE: WA
;          COUNTRY: USA
;          ZIP: 98101
;
;  COMPUTER READABLE FORM:
;          MEDIUM TYPE: Floppy disk
;          COMPUTER: Apple Power Macintosh
;          OPERATING SYSTEM: Apple Operating System 7.5.5
;          SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;
;  CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/09/871,856
;          FILING DATE: 31-May-2001
;          CLASSIFICATION: <Unknown>
;
;  PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: 08/996,139
;          FILING DATE: <Unknown>
;          APPLICATION NUMBER: USSN 08/813,509
;          FILING DATE: 07 MARCH 1997
;          APPLICATION NUMBER: USSN 08/772,330
;          FILING DATE: 23 DECEMBER 1996
;
;  ATTORNEY/AGENT INFORMATION:
;          NAME: Perkins, Patricia Anne
;          REGISTRATION NUMBER: 34,693
;          REFERENCE/DOCKET NUMBER: 2851-A
;
;  TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (206)587-0430
;          TELEFAX: (206)233-0644
;
;  INFORMATION FOR SEQ ID NO: 13:
;          SEQUENCE CHARACTERISTICS:
;              LENGTH: 317 amino acids
;              TYPE: amino acid
;              TOPOLOGY: linear
;          MOLECULE TYPE: protein
;          SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-871-856-13

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Query Match          100.0%;  Score 1685;  DB 9;  Length 317;
Best Local Similarity 100.0%;  Pred. No. 1.2e-155;
Matches 317;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQMV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQMV 240

```

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300  
 |||  
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300  
 |||  
 Qy 301 PDQDATYFGAFKVRDID 317  
 |||  
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 3

US-09-877-650-13

; Sequence 13, Application US/09877650

; Patent No. US20020169117A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/877,650

; FILING DATE: 08-Jun-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/995,659

; FILING DATE: 1997-12-22

; APPLICATION NUMBER: USSN 08/813,509

; FILING DATE: 07 MARCH 1997

; APPLICATION NUMBER: USSN 08/772,330

; FILING DATE: 23 DECEMBER 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia Anne

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2852-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206)587-0430

; TELEFAX: (206)233-0644

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 317 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-877-650-13



Query Match 100.0%; Score 1685; DB 9; Length 317;  
Best Local Similarity 100.0%; Pred. No. 1.2e-155;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
      |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
      |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFahLTINATDIPSGSH 180
      |||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFahLTINATDIPSGSH 180

Qy    181 KVSLSWYHdRGWAKISNMtFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYlQLMV 240
      |||
Db    181 KVSLSWYHdRGWAKISNMtFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYlQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEfHFYSINVGgFFKLRSgEEISIEVSNPSLLD 300
      |||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEfHFYSINVGgFFKLRSgEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
      |||
Db    301 PDQDATYFGAFKVRDID 317
```

RESULT 4

US-10-289-456-79

; Sequence 79, Application US/10289456

; Publication No. US20040033211A1

; GENERAL INFORMATION:

; APPLICANT: Bachmann, Martin

; APPLICANT: Maurer, Patrick

; APPLICANT: Spohn, Gunther

; TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease

; FILE REFERENCE: 1700.0330001

; CURRENT APPLICATION NUMBER: US/10/289,456

; CURRENT FILING DATE: 2002-11-07

; PRIOR APPLICATION NUMBER: PCT/IB02/00166

; PRIOR FILING DATE: 2002-01-21

; PRIOR APPLICATION NUMBER: US 10/050,902

; PRIOR FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: US 60/396,635

; PRIOR FILING DATE: 2002-07-19

; PRIOR APPLICATION NUMBER: US 60/331,045

; PRIOR FILING DATE: 2001-11-07

; NUMBER OF SEQ ID NOS: 170

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 79

; LENGTH: 317

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-289-456-79

Query Match 100.0%; Score 1685; DB 12; Length 317;  
Best Local Similarity 100.0%; Pred. No. 1.2e-155;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDIAKRSKLEAQPFahLTINATDIPSGSH 180
        |||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDIAKRSKLEAQPFahLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
        |||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        |||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
        |||
Db    301 PDQDATYFGAFKVRDID 317
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RESULT 5

US-10-202-062-22

; Sequence 22, Application US/10202062

; Publication No. US20040038349A1

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc.,

; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members

; FILE REFERENCE: PF559

; CURRENT APPLICATION NUMBER: US/10/202,062

; CURRENT FILING DATE: 2002-07-25

; PRIOR APPLICATION NUMBER: 60/307,838

; PRIOR FILING DATE: 2001-07-27

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 22

; LENGTH: 317

; TYPE: PRT

; ORGANISM: human

US-10-202-062-22

Query Match 100.0%; Score 1685; DB 12; Length 317;  
Best Local Similarity 100.0%; Pred. No. 1.2e-155;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
```

Qy 61 VCSVALFFYFRAQMDPNRISEGDTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
 |||  
 Db 61 VCSVALFFYFRAQMDPNRISEGDTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy 121 QAFQGA VQKELQHIVGSQHIRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180  
 |||  
 Db 121 QAFQGA VQKELQHIVGSQHIRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240  
 |||  
 Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300  
 |||  
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317  
 |||  
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 6

US-09-865-363-13

; Sequence 13, Application US/09865363

; Publication No. US20020086826A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/865,363

; FILING DATE: 25-May-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/995,659

; FILING DATE: <Unknown>

; APPLICATION NUMBER: USSN 08/813,509

; FILING DATE: 07 MARCH 1997

; APPLICATION NUMBER: USSN 08/772,330

; FILING DATE: 23 DECEMBER 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia Anne

```

;          REGISTRATION NUMBER: 34,693
;          REFERENCE/DOCKET NUMBER: 2852-A
;          TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (206)587-0430
;          TELEFAX: (206)233-0644
;          INFORMATION FOR SEQ ID NO: 13:
;          SEQUENCE CHARACTERISTICS:
;          LENGTH: 317 amino acids
;          TYPE: amino acid
;          TOPOLOGY: linear
;          MOLECULE TYPE: protein
;          SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-865-363-13

```

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Query Match          100.0%;  Score 1685;  DB 12;  Length 317;
Best Local Similarity 100.0%;  Pred. No. 1.2e-155;
Matches 317;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
        |||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
        |||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        |||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
        |||
Db    301 PDQDATYFGAFKVRDID 317

```

# RESULT 7

US-10-151-071-10

```

; Sequence 10, Application US/10151071
; Publication No. US20030017151A1
; GENERAL INFORMATION:
; APPLICANT: DOUGALL, William
; APPLICANT: ANDERSON, Dirk
; TITLE OF INVENTION: THERAPEUTIC USES OF RANK ANTAGONISTS
; FILE REFERENCE: 3277-A
; CURRENT APPLICATION NUMBER: US/10/151,071
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/291,919
; PRIOR FILING DATE: 2001-05-17
; NUMBER OF SEQ ID NOS: 10

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; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 317  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-151-071-10

Query Match 100.0%; Score 1685; DB 12; Length 317;  
Best Local Similarity 100.0%; Pred. No. 1.2e-155;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
|  
Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
  
Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
|  
Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
  
Qy 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPFHAHLTINATDIPSGSH 180  
|  
Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPFHAHLTINATDIPSGSH 180  
  
Qy 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240  
|  
Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240  
  
Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300  
|  
Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300  
  
Qy 301 PDQDATYFGAFKVRDID 317  
|  
Db 301 PDQDATYFGAFKVRDID 317

RESULT 8

US-09-957-944-6

; Sequence 6, Application US/09957944  
; Publication No. US20020086312A1  
; GENERAL INFORMATION:  
; APPLICANT: Dougall, William C.  
; TITLE OF INVENTION: SCREENING ASSAYS FOR AGONISTS AND ANTAGONISTS OF RECEPTOR  
ACTIVATOR OF  
; TITLE OF INVENTION: NF-kappa B  
; FILE REFERENCE: 3109-A  
; CURRENT APPLICATION NUMBER: US/09/957,944  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/235,157  
; PRIOR FILING DATE: 2000-09-22  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 317  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-957-944-6

Query Match 100.0%; Score 1685; DB 12; Length 317;  
Best Local Similarity 100.0%; Pred. No. 1.2e-155;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180
        |||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180

Qy    181 KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQIMV 240
        |||
Db    181 KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQIMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        |||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
        |||
Db    301 PDQDATYFGAFKVRDID 317
```

RESULT 9

US-10-218-547-22

; Sequence 22, Application US/10218547

; Publication No. US20030100074A1

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc.

; TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Relating To

; TITLE OF INVENTION: Human Endokine Alpha

; FILE REFERENCE: PF561

; CURRENT APPLICATION NUMBER: US/10/218,547

; CURRENT FILING DATE: 2002-08-15

; PRIOR APPLICATION NUMBER: 60/312,542

; PRIOR FILING DATE: 2001-08-16

; PRIOR APPLICATION NUMBER: 60/330,761

; PRIOR FILING DATE: 2001-10-30

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 22

; LENGTH: 317

; TYPE: PRT

; ORGANISM: human

US-10-218-547-22

Query Match 100.0%; Score 1685; DB 14; Length 317;  
Best Local Similarity 100.0%; Pred. No. 1.2e-155;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
 |||  
 Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
 |||  
 Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
 |||  
 Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
 |||  
 Qy 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180  
 |||  
 Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180  
 |||  
 Qy 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQMV 240  
 |||  
 Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQMV 240  
 |||  
 Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300  
 |||  
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300  
 |||  
 Qy 301 PDQDATYFGAFKVRDID 317  
 |||  
 Db 301 PDQDATYFGAFKVRDID 317  
 |||

RESULT 10

US-10-405-878-13

; Sequence 13, Application US/10405878

; Publication No. US20030175840A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/405,878

; FILING DATE: 01-Apr-2003

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/996,139

; FILING DATE: 22 DECEMBER 1997

; APPLICATION NUMBER: USSN 60/064,671

; FILING DATE: 14 OCTOBER 1997

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;          APPLICATION NUMBER: USSN 08/813,509
;          FILING DATE: 07 MARCH 1997
;          APPLICATION NUMBER: USSN 08/772,330
;          FILING DATE: 23 DECEMBER 1996
;          ATTORNEY/AGENT INFORMATION:
;          NAME: Perkins, Patricia Anne
;          REGISTRATION NUMBER: 34,693
;          REFERENCE/DOCKET NUMBER: 2851-A
;          TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (206)587-0430
;          TELEFAX: (206)233-0644
;          INFORMATION FOR SEQ ID NO: 13:
;          SEQUENCE CHARACTERISTICS:
;          LENGTH: 317 amino acids
;          TYPE: amino acid
;          TOPOLOGY: linear
;          MOLECULE TYPE: protein
;          SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-405-878-13

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Query Match          100.0%;  Score 1685;  DB 14;  Length 317;
Best Local Similarity 100.0%;  Pred. No. 1.2e-155;
Matches 317;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHPQPPAASRSMFVALLGLGLGQV 60
        |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHPQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGA VQKELQHIVGSQHIRAEKAMVDG SWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180
        |||
Db    121 QAFQGA VQKELQHIVGSQHIRAEKAMVDG SWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
        |||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        |||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
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Db    301 PDQDATYFGAFKVRDID 317

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# RESULT 11

US-10-167-182-11

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; Sequence 11, Application US/10167182
; Publication No. US20030176647A1
; GENERAL INFORMATION:
; APPLICANT: Yamaguchi, Kyoji
; APPLICANT: Yasuda, Hisataka
; APPLICANT: Nakagawa, No. US20030176647A1uaki

```



```

; APPLICANT: Shima, No. US20030176647A1uyuki
; APPLICANT: Kinosaki, Masahiko
; APPLICANT: Tsuda, Eisuke
; APPLICANT: Goto, Masaaki
; APPLICANT: Yano, Kazuki
; APPLICANT: Tomoyasu, Akihiro
; APPLICANT: Kobayashi, Fumie
; APPLICANT: Washida, Naohiro
; APPLICANT: Takahashi, Ken
; APPLICANT: Morinaga, Tomonori
; APPLICANT: Higashio, Kanji
; TITLE OF INVENTION: Antibodies to OCIF-binding Molecules
; FILE REFERENCE: FJN-070DV
; CURRENT APPLICATION NUMBER: US/10/167,182
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 09/202,455
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: JP 97808/1997
; PRIOR FILING DATE: 1997-04-15
; PRIOR APPLICATION NUMBER: JP 151434/1997
; PRIOR FILING DATE: 1997-06-09
; PRIOR APPLICATION NUMBER: JP 217897/1997
; PRIOR FILING DATE: 1997-08-12
; PRIOR APPLICATION NUMBER: JP 224803/1997
; PRIOR FILING DATE: 1997-08-21
; PRIOR APPLICATION NUMBER: JP 332241/1997
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: WO PCT/JP98/01728
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-167-182-11

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Query Match          100.0%; Score 1685; DB 14; Length 317;
Best Local Similarity 100.0%; Pred. No. 1.2e-155;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFALHTINATDIPSGSH 180
        |||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFALHTINATDIPSGSH 180

Qy    181 KVSLSWYHNRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
        |||
Db    181 KVSLSWYHNRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

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Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300  
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 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300  
 Qy 301 PDQDATYFGAFKVRDID 317  
 |||  
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 12

US-10-310-793-28

; Sequence 28, Application US/10310793

; Publication No. US20030198640A1

; GENERAL INFORMATION:

; APPLICANT: Yu, Guo-Liang

; APPLICANT: Ni, Jian

; APPLICANT: Rosen, Craig A

; APPLICANT: Zhang, Jun

; APPLICANT: Wei, Ping

; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases

; TITLE OF INVENTION: Relating To Human Tumor Necrosis Factor-Gamma Beta

; FILE REFERENCE: PF573

; CURRENT APPLICATION NUMBER: US/10/310,793

; CURRENT FILING DATE: 2002-12-06

; PRIOR APPLICATION NUMBER: 60/336,695

; PRIOR FILING DATE: 2001-12-07

; PRIOR APPLICATION NUMBER: 10/226,294

; PRIOR FILING DATE: 2002-08-23

; PRIOR APPLICATION NUMBER: 60/314,381

; PRIOR FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: 09/899,059

; PRIOR FILING DATE: 2001-07-06

; PRIOR APPLICATION NUMBER: 60/278,449

; PRIOR FILING DATE: 2001-03-26

; PRIOR APPLICATION NUMBER: 60/216,879

; PRIOR FILING DATE: 2000-07-07

; PRIOR APPLICATION NUMBER: 09/559,290

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: 60/180,908

; PRIOR FILING DATE: 2000-02-08

; PRIOR APPLICATION NUMBER: 60/134,067

; PRIOR FILING DATE: 1999-05-13

; PRIOR APPLICATION NUMBER: 60/132,227

; PRIOR FILING DATE: 1999-05-03

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 71

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 28

; LENGTH: 317

; TYPE: PRT

; ORGANISM: human

US-10-310-793-28

Query Match 100.0%; Score 1685; DB 14; Length 317;

Best Local Similarity 100.0%; Pred. No. 1.2e-155;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
 |||  
 Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
 |||  
 Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHLTINATDIPSGSH 180  
 |||  
 Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHLTINATDIPSGSH 180

Qy 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240  
 |||  
 Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300  
 |||  
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317  
 |||  
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 13

US-10-460-623-11

; Sequence 11, Application US/10460623

; Publication No. US20030208045A1

; GENERAL INFORMATION:

; APPLICANT: Yamaguchi, Kyoji

; APPLICANT: Yasuda, Hisataka

; APPLICANT: Nakagawa, No. US20030208045A1uaki

; APPLICANT: Shima, No. US20030208045A1uyuki

; APPLICANT: Kinosaki, Masahiko

; APPLICANT: Tsuda, Eisuke

; APPLICANT: Goto, Masaaki

; APPLICANT: Yano, Kazuki

; APPLICANT: Tomoyasu, Akihiro

; APPLICANT: Kobayashi, Fumie

; APPLICANT: Washida, Naohiro

; APPLICANT: Takahashi, Ken

; APPLICANT: Morinaga, Tomonori

; APPLICANT: Higashio, Kanji

; TITLE OF INVENTION: No. US20030208045A1el Protein and Method for Producing the Protein

; FILE REFERENCE: FJN-070

; CURRENT APPLICATION NUMBER: US/10/460,623

; CURRENT FILING DATE: 2003-06-13

; PRIOR APPLICATION NUMBER: JP 97808/1997

; PRIOR FILING DATE: 1997-04-15

; PRIOR APPLICATION NUMBER: JP 151434/1997

; PRIOR FILING DATE: 1997-06-09

; PRIOR APPLICATION NUMBER: JP 217897/1997

; PRIOR FILING DATE: 1997-08-12

; PRIOR APPLICATION NUMBER: JP 224803/1997

; PRIOR FILING DATE: 1997-08-21  
; PRIOR APPLICATION NUMBER: JP 332241/1997  
; PRIOR FILING DATE: 1997-12-02  
; PRIOR APPLICATION NUMBER: WO PCT/JP98/01728  
; PRIOR FILING DATE: 1998-04-15  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 317  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-460-623-11

Query Match 100.0%; Score 1685; DB 15; Length 317;  
Best Local Similarity 100.0%; Pred. No. 1.2e-155;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV	60
Db	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV	60
Qy	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Db	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Qy	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH	180
Db	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH	180
Qy	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQMV	240
Db	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQMV	240
Qy	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD	300
Db	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD	300
Qy	301	PDQDATYFGAFKVRDID	317
Db	301	PDQDATYFGAFKVRDID	317

RESULT 14

US-10-664-801-2

; Sequence 2, Application US/10664801  
; Publication No. US20040115199A1  
; GENERAL INFORMATION:  
; APPLICANT: M&E Biotech A/S  
; APPLICANT: HALKIER, Torben  
; APPLICANT: HAANING, Jesper  
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand  
; TITLE OF INVENTION: Activity  
; FILE REFERENCE: 22021 PC 1  
; CURRENT APPLICATION NUMBER: US/10/664,801  
; CURRENT FILING DATE: 2003-09-17  
; PRIOR APPLICATION NUMBER: US/09/396,937  
; PRIOR FILING DATE: 1999-09-15

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; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 317
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-664-801-2
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Qy	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAHQPPAASRSMFVALLGLGLGQV	60
Db	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAHQPPAASRSMFVALLGLGLGQV	60
Qy	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Db	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Qy	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH	180
Db	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH	180
Qy	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQMV	240
Db	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQMV	240
Qy	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD	300
Db	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD	300
Qy	301	PDQDATYFGAFKVRDID	317
Db	301	PDQDATYFGAFKVRDID	317

Query Match 100.0%; Score 1685; DB 16; Length 317;  
Best Local Similarity 100.0%; Pred. No. 1.2e-155;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHLTINATDIPSGSH 180
          ||||||||||||||||||||||||||||||||||||||||||||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQMV 240
          ||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
          ||||||||||||||||||||||||||||||||||||||||||||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
          |||||||
Db    301 PDQDATYFGAFKVRDID 317
```

Search completed: September 15, 2004, 09:01:41  
Job time : 673 secs

OM protein - protein search, using sw model

Run on: September 15, 2004, 08:32:23 ; Search time 116 Seconds  
(without alignments)  
862.235 Million cell updates/sec

Title: US-09-211-315-39  
Perfect score: 1685  
Sequence: 1 MRRASRDYTKYLRGSEEMGG.....LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query	
No.	Score	Match Length DB ID Description
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1	266	15.8	317	13	Q7ZYX9	Q7zyx9 brachydanio
2	265	15.7	304	13	Q7T1F2	Q7t1f2 gallus gall
3	240.5	14.3	214	13	Q9DDZ5	Q9ddz5 brachydanio
4	216.5	12.8	287	13	Q90WT9	Q90wt9 gallus gall
5	215.5	12.8	287	11	Q8K3G0	Q8k3g0 rattus norv
6	194.5	11.5	280	6	Q861W5	Q861w5 felis silve
7	187.5	11.1	279	11	Q7TMV9	Q7tmv9 mus musculu
8	184.5	10.9	252	11	Q8K3Y8	Q8k3y8 mus musculu
9	179.5	10.7	252	11	Q80YZ0	Q80yz0 mus musculu
10	177.5	10.5	252	11	Q8K3Y7	Q8k3y7 rattus norv
11	156.5	9.3	251	4	Q8NFE9	Q8nfe9 homo sapien
12	139.5	8.3	215	11	Q99ND1	Q99nd1 tamiasciuru
13	137.5	8.2	156	11	Q91ZL4	Q91zl4 sigmodon hi
14	137.5	8.2	232	11	Q80XA4	Q80xa4 peromyscus
15	133	7.9	149	6	O97543	O97543 aotus nancy
16	131.5	7.8	216	11	O70332	O70332 mesocricetu
17	130	7.7	217	11	Q9ERG6	Q9erg6 peromyscus
18	127.5	7.6	217	6	Q9BEC5	Q9bec5 tenrec ecau
19	126	7.5	149	6	O97538	O97538 aotus vocif
20	126	7.5	149	6	Q9TTG8	Q9ttg8 aotus nigri
21	126	7.5	302	11	Q7TSL5	Q7tsl5 peromyscus
22	125	7.4	216	6	Q9BEC9	Q9bec9 ochotona pr
23	120.5	7.2	217	6	Q9BEG0	Q9beg0 cyclopes di
24	120.5	7.2	217	6	Q9BEG1	Q9beg1 bradypus tr
25	118.5	7.0	138	6	Q9TTG7	Q9ttg7 aotus lemur
26	117	6.9	244	6	Q862Z7	Q862z7 pan troglod
27	116.5	6.9	169	11	Q9WV90	Q9wv90 marmota mon
28	115.5	6.9	154	6	Q8MJ19	Q8mj19 macaca mula
29	114.5	6.8	216	6	Q9BEE0	Q9bee0 macropus ru
30	113.5	6.7	216	6	Q9BEC4	Q9bec4 talpa europ
31	113.5	6.7	237	13	Q8AWC9	Q8awc9 cyprinus ca
32	113	6.7	217	6	Q9BEF4	Q9bef4 cabassous u
33	111	6.6	102	11	Q80Z03	Q80z03 castor cana
34	110.5	6.6	215	6	Q9BEE8	Q9bee8 erinaceus e
35	110	6.5	102	11	Q80Z02	Q80z02 trichys fas
36	109.5	6.5	253	13	Q7T194	Q7t194 acanthopagr
37	109	6.5	102	11	Q80Z05	Q80z05 dipodomys m
38	108	6.4	102	11	Q80Z06	Q80z06 dipus sagit
39	107.5	6.4	222	13	Q7T1U4	Q7t1u4 pagrus majo
40	107.5	6.4	409	5	Q8MY88	Q8my88 drosophila
41	107.5	6.4	409	5	Q8IGD3	Q8igd3 drosophila
42	106.5	6.3	325	5	Q9V5G2	Q9v5g2 drosophila
43	106.5	6.3	415	5	Q8MUJ1	Q8muj1 drosophila
44	106	6.3	3467	5	Q8I218	Q8i218 plasmodium
45	105.5	6.3	103	6	Q864Z0	Q864z0 physeter ca

# ALIGNMENTS

## RESULT 1

Q7ZYX9

ID Q7ZYX9 PRELIMINARY; PRT; 317 AA.

AC Q7ZYX9;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)





OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Sayed A.A., Horiuchi H.H., Furusawa S., Matsuda H.;  
 RT "Identification and Characterization of Chicken TNF-Superfamily  
 RT Ligand 8 (CD30 Ligand) and 10 (Tumor Necrosis Factor Related Apoptosis  
 RT Inducing Ligand TRAIL).";  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AB114678; BAC79267.1; -.  
 SQ SEQUENCE 304 AA; 34658 MW; DFC128B517747C96 CRC64;

Query Match 15.7%; Score 265; DB 13; Length 304;  
 Best Local Similarity 27.3%; Pred. No. 1.6e-15;  
 Matches 82; Conservative 56; Mismatches 126; Indels 36; Gaps 12;

Qy 38 PHQPPAASRSMFVALLGLGLGQVVCVALFFYFRAQMDP--NRISEDGTHCI--YRILRL 93  
 | | : : : | : | | | : | | : : | | | : : |  
 Db 3 PAGGPSAHTCGAVLVAAVLLQSVCAVVTYIYFTNELKQLWDITYSRSGTACLTGEELGDL 62

Qy 94 HENADFQDTTLESQDTKLIPDSCRRIKQAFQGAQVQKELQHIVGSQHIRAEKAMVDGSWLD 153  
 : | | : | : | : | | : : | : : | : : : : |  
 Db 63 IQNLD----VVESKDR--VADPCWQVKWHLGKLIKMMMSRI-----LQENMSAINGDRTQ 111

Qy 154 -LAKRSKLEAQP----FAHLTINATDIPSGSHKV-----SLSSWYHD-RGWAKISNM 199  
 | : : | : | | | : : : | : | | : : | : : | :  
 Db 112 ALSRRDEPPQGPTLRIAAHLTGSSKRSSASPHNYLSYRGIGHKIHWSERRGHSFLYNV 171

Qy 200 TFSNGKLIVNQDGFYYLYANICFRHHET----SG--DLATEYLQLMVVYVTKTSIKIPSSH 253  
 | : : | : | | | : : | | | : : | : | : | : | :  
 Db 172 ELWNGELVVPQTGFYYIYSQTYFRFRENEDEDSGLLERIKNPKQLVQYIYKLT-NYPDPI 230

Qy 254 TLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEESIEVSNPSLLDPDQDATYFGAFKV 313  
 | | | | : | : | : | : | : | : | : | : | : | : | :  
 Db 231 LLMKSARTSCWSKKAELYGVYQGGVFQLKREDRIFVSVSNSDIVDMDKEASFFGAFMI 290

# RESULT 3

Q9DDZ5

ID Q9DDZ5 PRELIMINARY; PRT; 214 AA.

AC Q9DDZ5;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE TRAIL-like protein.

GN TNFSF10L.

OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI\_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A.

RA Bobe J., Goetz F.W.;  
 RT "Molecular cloning and expression of a TNF receptor and two TNF  
 RT ligands in the fish ovary."  
 RL Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).  
 DR EMBL; AF250041; AAG47640.1; -.  
 DR HSSP; P50591; 1D2Q.  
 DR ZFIN; ZDB-GENE-010801-1; tnfsf10l.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 SQ SEQUENCE 214 AA; 24093 MW; 98C002474FF691AA CRC64;

Query Match 14.3%; Score 240.5; DB 13; Length 214;  
 Best Local Similarity 28.6%; Pred. No. 1.6e-13;  
 Matches 61; Conservative 50; Mismatches 83; Indels 19; Gaps 5;

Qy 118 RIKQAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAK-RSKLEAQPF AHLTINATDIP 176  
 : : : : : | : | : | : : | : : : | ||| : :  
 Db 2 KLAEGIKAYISKV TDSIISKQTLHAARTQTHSYNTTGSKFMTTVMQRP SAHLTLSSASDN 61  
  
 Qy 177 S-----GSHKVSLS SWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICF 222  
 | : : : | : | : ||| : || : | ||| ||| : : |  
 Db 62 SRPQSDMHQPQFDLHQSCRHPVHTWANKSFGAHLNMTLTNGRLRVPQDGRYYLYSQVYF 121  
  
 Qy 223 RHHETS-GDLATEY LQLMVYV-TKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGF 280  
 | : | : : || : ||| : ||| : ||| : || : : : : : : ||  
 Db 122 RYPSPSDSDQSSVSHQLVQCIYKKT SYLNPIQ--LLKGVGTKCWAPDAEYALHSVYQGGL 179  
  
 Qy 281 FKLRSGE EISIEVSNPSLLDPDQDATYFGAFKV 313  
 | : || : | : : || : || : : : : : : ||| : :  
 Db 180 FELRAGDEVFVSVSSPTMVYGEDSSSYFGAFRL 212

#### RESULT 4

Q90WT9

ID Q90WT9 PRELIMINARY; PRT; 287 AA.  
 AC Q90WT9;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE TNF-related apoptosis inducing ligand.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bridgham J.T., Johnson A.L.;  
 RT "TNF-related apoptosis inducing ligand (TRAIL) expression in the hen

RT ovary.";  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY057941; AAL23702.1; -.  
 DR HSSP; O35235; 1IQA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR006053; TNF\_abc.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 SQ SEQUENCE 287 AA; 32092 MW; DB06E1C95087B108 CRC64;

Query Match 12.8%; Score 216.5; DB 13; Length 287;  
 Best Local Similarity 24.7%; Pred. No. 3.5e-11;  
 Matches 61; Conservative 57; Mismatches 104; Indels 25; Gaps 6;

Qy 80 SEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQH 139  
 | : | : | : | : : : : : | : : : : :  
 Db 51 SSEELRCLQLINQQQEGSNLEEL-----ISNQSLKLANTIKAYVATVTENVISRSV 102

Qy 140 I-RAEKAMVDGSWLDLAKRSKLEAQPFahlTINATDIP-----SGSHKVSLSW 187  
 : : | : : : | : | : | : : : : : : : : : : :  
 Db 103 VNEAQKSYFNISEGQVA--TKTLGKPSAHLIFRPQNPAQDGSSRRFGNLSQSCRHAITRW 160

Qy 188 YHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVT-KTS 246  
 : : | : : : | : | : | : | : | : : : : : : : : : : :  
 Db 161 EDSTIHSHLQNITYRDGRLRVNQAGKYYVYSQIYFRYSRDGAGARVSVPLVQCINWKTS 220

Qy 247 IKIPSSHTLMKGGSTKYWSGNSEHFYSINVGGFKLRSGEIEISIEVSNPSLLDPDQDAT 306  
 | : | : | : | : : : : : | : | : : : : : : : : : : :  
 Db 221 YSQPI--LLLKGVGTKCWAPEAEYGLHALYQGGFLFELKAGDELFSVSVSSLAIDYSDAAS 278

Qy 307 YFGAFKV 313  
 | : | : | :  
 Db 279 YFGAFRL 285

# RESULT 5

Q8K3G0

ID Q8K3G0 PRELIMINARY; PRT; 287 AA.  
 AC Q8K3G0;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE TNF-related apoptosis inducing ligand.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.





RESULT 7

Q7TMV9

ID Q7TMV9 PRELIMINARY; PRT; 279 AA.  
 AC Q7TMV9;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Tnfsf6 protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;  
 RA Strausberg R.;  
 RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC052866; AAH52866.1; -.  
 SQ SEQUENCE 279 AA; 31416 MW; C2972E2728FBBB7B CRC64;

Query Match 11.1%; Score 187.5; DB 11; Length 279;  
 Best Local Similarity 21.7%; Pred. No. 1.4e-08;  
 Matches 70; Conservative 46; Mismatches 105; Indels 101; Gaps 11;

Qy 13 RGSEEMGGGPGAPHEGPHAPPPAPHP-----PAASRSMFVALLGLGL 57  
 || :: | | || | | | | : |||:|  
 Db 38 RGPDQRRPPPPPPVSPPLPPPSQPLPLPPLTPLKKKDHNTNLWLPVVFFMVLVALVGMGL 97  
 Qy 58 GQVVCVSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCR 117  
 | :|:: |  
 Db 98 G-----MYQLFHL----- 105

Qy 118 RIKQAFQGAVQKELQHI--VGSQHRA---EKAMVDGSWLDLAKRSKLEAQPFHAHLTINA 172  
 |||| : :| :: || : : | | : |||| |  
 Db 106 -----QKELAEELREFTNQSLKVSSFQKQIANPS----TPSEKKEPRSVVAHLTGN- 150  
 Qy 173 TDIPSGSHKVSLS-SWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 231  
 | | : | | || : : | | :: | | :: | : || :  
 Db 151 -----PHSRSIPLIEWEDTYGTALISGVKYKKGGLVINETGLYFVYSKVYFRGQSCN--- 201  
 Qy 232 ATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESI 291  
 : | || : : | | || : : : : | : | : : :  
 Db 202 -NQPLNHKVYMRNS--KYPEDLVLMEEKRLNYCT-TGQIWAHSSHLGAVFNLTADHLYV 257  
 Qy 292 EVSNPSLLDPDQDATYFGAFKV 313  
 : | || : : : | : | : :  
 Db 258 NISQLSLINFEEKSTFFGLYKL 279

RESULT 8

Q8K3Y8

ID Q8K3Y8 PRELIMINARY; PRT; 252 AA.  
 AC Q8K3Y8;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE TNF superfamily ligand TL1A.  
 GN TNFSF15.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RX MEDLINE=21909416; PubMed=11911831;  
 RA Migone T.S., Zhang J., Luo X., Zhuang L., Chen C., Hu B., Hong J.S.,  
 RA Perry J.W., Chen S.F., Zhou J.X., Cho Y.H., Ullrich S., Kanakaraj P.,  
 RA Carrell J., Boyd E., Olsen H.S., Hu G., Pukac L., Liu D., Ni J.,  
 RA Kim S., Gentz R., Feng P., Moore P.A., Ruben S.M., Wei P.;  
 RT "TL1A is a TNF-like ligand for DR3 and TR6/DcR3 and functions as a T  
 RT cell costimulator.";  
 RL Immunity 16:479-492(2002).  
 DR EMBL; AF520786; AAM77367.1; -.  
 DR MGD; MGI:2180140; Tnfsf15.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR006053; TNF\_abc.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 SQ SEQUENCE 252 AA; 27723 MW; BB901C9350119E0F CRC64;



Query Match 10.9%; Score 184.5; DB 11; Length 252;  
 Best Local Similarity 26.2%; Pred. No. 2.3e-08;  
 Matches 64; Conservative 39; Mismatches 100; Indels 41; Gaps 10;

```

Qy      105 ESQDTKLIPDSCRRIKQAFQGAVQK-----ELQHIVG-SQHIRAEKAMVDGSW 151
      |   ::||: ||   :|   |   :   : ||   :| :   ||
Db      11 EGVPEVLPEGCRHRPEARAGLAARSKACLAALTCCLLSFPILAGLSTLLMAGQLRVPGK- 69

Qy      152 LDLAKRKLE-----AQPF AHLTI-NATDIPSGSHKVSLSWYHDRGWAK 195
      |   |: |   :| |||||   |   |   ::|   ||| |
Db      70 -DCMLRAITEERSESPQQVYSPPRGKPRAH LTIKKQTPAPHLKNQLSALHWEHDLGMAF 128

Qy      196 ISN-MTFSNGKLIVNQDGFYYLYANICFR-HHETSGDLA-----TEYLQLMVYVTKTSIK 248
      | | : |   |:: : | |::|: | ||   ||::   :   : | :|| :
Db      129 TKNGMKYINKSLVIPESGDYFIYSQITFRGTTSVCGDISRGRRPKNKPD SITV VITKVADS 188

Qy      249 IPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD-PDQDATY 307
      |   |: |   :   |: | |: :| | |   |: : : ||: ||:|   :| |:
Db      189 YPEPARLLTGSKSVCEISNN--WFQSLYLGAMFSLEEGRMLMVNVSDISLVDYTKEDKTF 246

Qy      308 FGAF 311
      ||||
Db      247 FGAF 250
  
```

# RESULT 9

Q80YZ0

```

ID   Q80YZ0          PRELIMINARY;          PRT;    252 AA.
AC   Q80YZ0;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   BM20K13.3 (Tumor necrosis factor (Ligand) superfamily, member
DE   15).
GN   TNFSF15.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sycamore N.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL691468; CAD83021.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR008983; TNF_like.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
  
```

SQ SEQUENCE 252 AA; 27725 MW; A63ABDCC9E969E0F CRC64;

Query Match 10.7%; Score 179.5; DB 11; Length 252;  
Best Local Similarity 25.8%; Pred. No. 6.5e-08;  
Matches 63; Conservative 40; Mismatches 100; Indels 41; Gaps 10;

```
QY      105 ESQDTKLIPDSCRRIKQAFQGAVQK-----ELQHIVG-SQHIRAEKAMVDGSW 151
      |   :::|: ||   :| |   :   : | |   : | : | |
Db      11 EGVPEVLPPEGCRHRPEARAGLAARSKACLAALTCCLLSFPILAGLSTLLMAGQLRVPGK- 69

QY      152 LDLAKRSKLE-----AQPF AHLTI-NATDIPSGSHKVSLSWYHDRGWAK 195
      |   |: |   :| ||||| | |   ::| | || | |
Db      70 -DCMLRAITEERSESPSQQVYSPPRGK PRAHLTIKKQTPAPHLKNQLSALHWEHDLGMAF 128

QY      196 ISN-MTFSNGKLIVNQDGFYLYLANICFR-HHETSGDLA-----TEYLQLMVYVTKTSIK 248
      | | : | |: : | |: : | ||   ||: :   :   : : || :
Db      129 TKNGMKYINKSLVIPESGDYFIYSQITFRGTTSVCGDISRGRRPKNKPSITMVITKVADS 188

QY      249 IPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLD-PDQDATY 307
      |   |: | :   |: | |: :| | | |: : : ||: ||:| : | |:
Db      189 YPEPARLLTGSKSVCEISNN--WFQSLYLGATFSLEEGDRLMVNVS DISLVDYTKEDKTF 246

QY      308 FGAF 311
      ||||
Db      247 FGAF 250
```

RESULT 10

Q8K3Y7

ID Q8K3Y7 PRELIMINARY; PRT; 252 AA.  
AC Q8K3Y7;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE TNF superfamily ligand TL1A.  
GN TNFSF15.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley;  
RX MEDLINE=21909416; PubMed=11911831;  
RA Migone T.S., Zhang J., Luo X., Zhuang L., Chen C., Hu B., Hong J.S.,  
RA Perry J.W., Chen S.F., Zhou J.X., Cho Y.H., Ullrich S., Kanakaraj P.,  
RA Carrell J., Boyd E., Olsen H.S., Hu G., Pukac L., Liu D., Ni J.,  
RA Kim S., Gentz R., Feng P., Moore P.A., Ruben S.M., Wei P.;  
RT "TL1A is a TNF-like ligand for DR3 and TR6/DcR3 and functions as a T  
RT cell costimulator."  
RL Immunity 16:479-492(2002).  
DR EMBL; AF520787; AAM77368.1; -.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR006053; TNF\_abc.  
DR InterPro; IPR006052; TNF\_family.



DR EMBL; AF520785; AAM77366.1; -.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR006053; TNF\_abc.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 SQ SEQUENCE 251 AA; 28087 MW; 65ED70E367E3446D CRC64;

Query Match 9.3%; Score 156.5; DB 4; Length 251;  
 Best Local Similarity 28.0%; Pred. No. 7.7e-06;  
 Matches 45; Conservative 33; Mismatches 66; Indels 17; Gaps 6;

Qy 163 QPFAHLT-INATDIPSGSHKVSLSWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANI 220  
 :| ||| : | : : | | :| | : : | : : :  
 Db 94 KPRAHLTVVRQTPTQHFKNQFPALHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQV 153  
 Qy 221 CFRHHETSGDLATEYLQ-----LMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFH 271  
 || : :| | : | :| : | | : | : :  
 Db 154 TFRGMTSE---CSEIRQAGRPNKPDSITVVITKVTDSTYPEPTQLLMGTSVCEVGSN--W 208  
 Qy 272 FYSINVGGFKLRSGEEISIEVSNPSLLD-PDQDATYFGAF 311  
 | | :| | :| : : : || : || : | :| |||  
 Db 209 FQPIYLGAMFSLQEGDKLMVNVSDISLVDYTKEDKTFFGAF 249

# RESULT 12

Q99ND1

ID Q99ND1 PRELIMINARY; PRT; 215 AA.  
 AC Q99ND1;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Tumor necrosis factor (Fragment).  
 GN TNFA.  
 OS Tamiasciurus hudsonicus (American red squirrel).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;  
 OC Tamiasciurus.  
 OX NCBI\_TaxID=10009;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA van Dijk M.A.M., de Jong W.W.;  
 RT "Indels indicate that rodents are monophyletic and lagomorphs are  
 RT their sister group."  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AJ286824; CAC28540.1; -.  
 DR HSSP; P06804; 2TNF.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.

DR InterPro; IPR006053; TNF\_abc.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 215 215  
 SQ SEQUENCE 215 AA; 23739 MW; 36441309CA5E9898 CRC64;

Query Match 8.3%; Score 139.5; DB 11; Length 215;  
 Best Local Similarity 26.5%; Pred. No. 0.00021;  
 Matches 40; Conservative 27; Mismatches 51; Indels 33; Gaps 5;

Qy 163 QPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANIC 221  
 :| ||: | |: | | | :| | : :| | || | :| :  
 Db 79 KPSVAHVANQTE-----EQLQWLSRRANALLANGMELIDNQLVVPADGLYLIYSQVL 130  
 Qy 222 FRHHETSGDLATEYLQLMVYVTK-----TSIKIPSSHTLMKGGSTKYWSGNSE 269  
 |: | : |: | |:: : :|| | : :| | |  
 Db 131 FK-----GQGCSYVLLTHTVSRFAVSQDKVNLLSAIKSPCPKESLEGAEFKPW----- 180  
 Qy 270 FHFYSINVGGFKLRSGEEISIEVSNPSLLD 300  
 : | :|| |:| : :| ||: || ||  
 Db 181 --YEPIYLGGVFELQKGDRLSAEVLNPSYLD 209

# RESULT 13

Q91ZL4

ID Q91ZL4 PRELIMINARY; PRT; 156 AA.  
 AC Q91ZL4;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Tumor necrosis factor alpha (Fragment).  
 OS Sigmodon hispidus (Hispid cotton rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;  
 OC Sigmodon.  
 OX NCBI\_TaxID=42415;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Blanco J.C., Pletneva L.M., Prince G.A.;  
 RT "Sigmodon hispidus cytokines, chemokines and interferons."  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF421388; AAL18818.1; -.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR006053; TNF\_abc.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.

DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 156 AA; 17303 MW; DC565F3BC3C826E4 CRC64;

Query Match 8.2%; Score 137.5; DB 11; Length 156;  
 Best Local Similarity 27.0%; Pred. No. 0.0002;  
 Matches 43; Conservative 25; Mismatches 68; Indels 23; Gaps 7;

Qy 160 LEAQPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYA 218  
 | :| ||: | | | | :| | | :| :| || | :| :  
 Db 8 LSDKPVAVHVAN-----QQAEEQLEWLSQRANALLANGMDLRNNQLVIPADGLYLVYS 60  
 Qy 219 NICFRHHETSG-DLATEYLQLMV--YVTK----TSIKIPSSHTLMKGGSTKYWSGNSEFH 271  
 : | : | :| | : : | | :| | | :| | |  
 Db 61 QVLFKGLGRSNCELLTHTVSRIAVSYEDKVNLLSAIKSPCPKETPQGAELKPW----- 113  
 Qy 272 FYSINVGGFKLRSGEESIEVSNPSLLD-PDQDATYFG 309  
 : | :| | :| | : :| ||:| || : |||  
 Db 114 YEPIYLGGVFQLEKGDRLSAEVNHPKYLDFAESGQVYFG 152

#### RESULT 14

##### Q80XA4

ID Q80XA4 PRELIMINARY; PRT; 232 AA.  
 AC Q80XA4;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Tumor necrosis factor precursor (Fragment).  
 GN TNF.  
 OS Peromyscus maniculatus (Deer mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;  
 OC Peromyscus.  
 OX NCBI\_TaxID=10042;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Green R.M., Herbst M.M., Schountz T.;  
 RT "Cloning of the deer mouse tumor necrosis factor gene."  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY249143; AAP03078.1; -.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR006053; TNF\_abc.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.

DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 KW Signal.  
 FT SIGNAL 1 20 Potential.  
 FT CHAIN 80 >232 tumor necrosis factor.  
 FT NON\_TER 232 232  
 SQ SEQUENCE 232 AA; 25704 MW; E48A9379DB4F216D CRC64;

Query Match 8.2%; Score 137.5; DB 11; Length 232;  
 Best Local Similarity 25.9%; Pred. No. 0.00036;  
 Matches 42; Conservative 27; Mismatches 58; Indels 35; Gaps 7;

QY 163 QPFAHLTINATDIPSGSHKVSLS-SWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANI 220  
 :| ||: | | :| | | :| | :| :| || | :| :  
 Db 90 KPVAVHVAN-----HQVDEQLEWLSRRANALLANGMDLKDNLQIVIPADGLYLVSQV 141  
 QY 221 CFRHHETSGDLATEYLQLMVYVTK-----TSIKIPSSHTLMKGGSTKYWSGNS 268  
 | : | : | :| :| :| | :| | |  
 Db 142 LFK-----GQGCSNYVLLTHTVSRFAVSIEDKVNLLSAIKSPCPKETPEGSELKPW---- 192  
 QY 269 EFHFYSINVGGFFKLRSGEEISIEVSNPSLLD-PDQDATYFG 309  
 : | :| | :| | : :| || : | | : |||  
 Db 193 ---YEPIYLGGVFQLEKGDRLSAEVNLPKYLDFAESGQVYFG 231

# RESULT 15

O97543

ID O97543 PRELIMINARY; PRT; 149 AA.  
 AC O97543;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Tumor necrosis factor alpha (Fragment).  
 GN TNF-ALPHA.  
 OS Aotus nancymaae (Ma's night monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.  
 OX NCBI\_TaxID=37293;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Echeverry S.J., Hernandez E., Moreno A., Patarroyo M.E., Murillo L.A.;  
 RT "Identification, cloning and sequencing of different interleukin genes  
 RT in 4 Aotus species.";  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF014513; AAD01539.1; -.  
 DR HSSP; P01375; 4TSV.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR006053; TNF\_abc.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.

DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 149 149  
 SQ SEQUENCE 149 AA; 16466 MW; 3C2A6140778EFA8A CRC64;

Query Match 7.9%; Score 133; DB 6; Length 149;  
 Best Local Similarity 25.5%; Pred. No. 0.00048;  
 Matches 40; Conservative 31; Mismatches 62; Indels 24; Gaps 8;

Qy 163 QPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANIC 221  
 :| ||: | : : | : | :| : : :| :| :| : :  
 Db 4 KPVAHVVAN----PQAEGQL---QWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVL 56  
 Qy 222 FRHH--ETSGDLATEYLQLMV--YVTK----TSIKIPSSHTLMKGGSTKYWSGNSEFHFY 273  
 |: : : | : : | || :|| | :| | | :  
 Db 57 FKGQGCPSHVLTLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPW-----YE 109  
 Qy 274 SINVGFFFKLRSGEIEISIEVSNPSLLD-PDQDATYFG 309  
 | :|| |:| |: :| |:: | || : |||  
 Db 110 PIYLGGVFQLEKGDRLSAEINRPDYLDFAESGQVYFG 146

Search completed: September 15, 2004, 08:38:37  
 Job time : 119 secs



OM protein - protein search, using sw model

Run on: September 15, 2004, 08:32:22 ; Search time 24 Seconds  
 (without alignments)  
 687.760 Million cell updates/sec

Title: US-09-211-315-39  
 Perfect score: 1685  
 Sequence: 1 MRRASRDYTKYLRGSEEMGG.....LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

# SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	1685	100.0	317	1	TN11_HUMAN	014788 h tumor nec	
2	1417.5	84.1	316	1	TN11_MOUSE	035235 m tumor nec	
3	1396.5	82.9	318	1	TN11_RAT	Q9ese2 r tumor nec	
4	251.5	14.9	281	1	TN10_HUMAN	P50591 homo sapien	
5	248	14.7	291	1	TN10_MOUSE	P50592 mus musculu	
6	200	11.9	282	1	TNF6_PIG	Q9bea8 sus scrofa	
7	189	11.2	281	1	TNF6_HUMAN	P48023 homo sapien	
8	186	11.0	280	1	TNF6_MACMU	Q9myl6 macaca mula	
9	184.5	10.9	279	1	TNF6_MOUSE	P41047 mus musculu	
10	182.5	10.8	280	1	TNF6_CERTO	Q9bdn1 cercocebus	
11	176.5	10.5	261	1	TNF5_BOVIN	P51749 bos taurus	
12	175.5	10.4	278	1	TNF6_RAT	P36940 rattus norv	
13	169.5	10.1	261	1	TNF5_CALJA	Q9bdn3 callithrix	
14	167.5	9.9	261	1	TNF5_AOTTR	Q9bdm3 aotus trivi	
15	158.5	9.4	261	1	TNF5_HUMAN	P29965 homo sapien	
16	155.5	9.2	261	1	TNF5_MACMU	Q9bdc7 macaca mula	
17	155	9.2	272	1	TNF5_CHICK	Q9i8d8 gallus gall	

18	152.5	9.1	261	1	TNF5_PIG	Q95mq5	sus scrofa
19	152	9.0	260	1	TNF5_FELCA	O97605	felis silve
20	146	8.7	234	1	TNFA_CAVPO	P51435	cavia porce
21	145.5	8.6	239	1	TN14_MOUSE	Q9qyh9	mus musculu
22	145	8.6	174	1	TN15_HUMAN	O95150	homo sapien
23	145	8.6	260	1	TNF5_CANFA	O97626	canis famil
24	143	8.5	240	1	TNF5_MACNE	Q9bdm7	macaca neme
25	141.5	8.4	235	1	TNFA_MOUSE	P06804	mus musculu
26	140.5	8.3	235	1	TNFA_RABIT	P04924	oryctolagus
27	139	8.2	233	1	TNFA_SAIISC	Q8mkg8	saimiri sci
28	137	8.1	234	1	TNFA_SHEEP	P23383	ovis aries
29	136	8.1	234	1	TNFA_CAPHI	P13296	capra hircu
30	134.5	8.0	310	1	TNFC_MARMO	Q9jml0	marmota mon
31	134	8.0	233	1	TNFA_MACFA	P79337	macaca fasc
32	134	8.0	240	1	TN14_HUMAN	O43557	homo sapien
33	133	7.9	232	1	TNFA_PANTR	Q8hzd9	pan troglod
34	133	7.9	233	1	TNFA_CANFA	P51742	canis famil
35	133	7.9	233	1	TNFA_HUMAN	P01375	homo sapien
36	133	7.9	233	1	TNFA_MACMU	P48094	macaca mula
37	132.5	7.9	235	1	TNFA_PERLE	P36939	peromyscus
38	131.5	7.8	235	1	TNFA_RAT	P16599	rattus norv
39	130.5	7.7	306	1	TNFC_MOUSE	P41155	mus musculu
40	130	7.7	233	1	TNFA_PAPSP	P33620	papio sp. (
41	129.5	7.7	233	1	TNFA_MARMO	O35734	marmota mon
42	129	7.7	233	1	TNFA_PAPAN	P59695	papio anubi
43	129	7.7	233	1	TNFA_PAPHU	O77510	papio hamad
44	128	7.6	234	1	TNFA_HORSE	P29553	equus cabal
45	126.5	7.5	233	1	TNFA_BOVIN	Q06599	bos taurus

# ALIGNMENTS

## RESULT 1

### TN11\_HUMAN

ID TN11\_HUMAN STANDARD; PRT; 317 AA.  
AC O14788; O14723; Q96Q17; Q9P2Q3;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator  
DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-  
DE induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast  
DE differentiation factor) (ODF).  
GN TNFSF11 OR RANKL OR TRANCE OR OPGL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Bone marrow, and Peripheral blood;  
RX MEDLINE=98032977; PubMed=9367155;  
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,  
RA Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,  
RA Galibert L.;  
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth

RT and dendritic-cell function.";

RL Nature 390:175-179(1997).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Lymph node;

RX MEDLINE=98227661; PubMed=9568710;

RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,

RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,

RA Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,

RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,

RA Boyle W.J.;

RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast

RT differentiation and activation.";

RL Cell 93:165-176(1998).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).

RA Ikeda T., Kuroyama H., Hirokawa K.;

RT "Determination of human RANKL isoforms.";

RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

RN [4]

RP SEQUENCE OF 73-317 FROM N.A.

RC TISSUE=Thymocytes;

RX MEDLINE=97460112; PubMed=9312132;

RA Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,

RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,

RA Choi Y.;

RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family

RT that activates c-Jun N-terminal kinase in T cells.";

RL J. Biol. Chem. 272:25190-25194(1997).

RN [5]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC TISSUE=Tongue;

RX MEDLINE=20175237; PubMed=10708588;

RA Nagai M., Kyakumoto S., Sato N.;

RT "Cancer cells responsible for humoral hypercalcemia express mRNA

RT encoding a secreted form of ODF/TRANCE that induces osteoclast

RT formation.";

RL Biochem. Biophys. Res. Commun. 269:532-536(2000).

CC -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to

CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.

CC Augments the ability of dendritic cells to stimulate naive T-cell

CC proliferation. May be an important regulator of interactions

CC between T cells and dendritic cells and may play a role in the

CC regulation of the T cell-dependent immune response. May also play

CC an important role in enhanced bone-resorption in humoral

CC hypercalcemia of malignancy.

CC -!- SUBUNIT: Homotrimer (By similarity).

CC -!- SUBCELLULAR LOCATION: Type II membrane protein (isoforms 1 and 3);

CC Secreted (isoform 2). A soluble form of isoform 1 arises by

CC proteolytic processing (By similarity).

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=3;

CC Name=1;

CC IsoId=O14788-1; Sequence=Displayed;

CC Name=2; Synonyms=SODF;

CC IsoId=O14788-2; Sequence=VSP\_006447;

CC Name=3;

```

CC      IsoId=O14788-3; Sequence=VSP_006446;
CC      -!- TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NODES BUT WEAK
CC          IN SPLEEN, PERIPHERAL BLOOD LEUKOCYTES, BONE MARROW, HEART,
CC          PLACENTA, SKELETAL MUSCLE, STOMACH AND THYROID.
CC      -!- INDUCTION: UPREGULATED BY T CELL RECEPTOR STIMULATION.
CC      -!- PTM: The soluble form of isoform 1 derives from the membrane form
CC          by proteolytic processing (By similarity). The cleavage may be
CC          catalyzed by ADAM17.
CC      -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF019047; AAB86811.1; -.
DR      EMBL; AF053712; AAC39731.1; -.
DR      EMBL; AB064269; BAB79694.1; -.
DR      EMBL; AB061227; BAB71768.1; -.
DR      EMBL; AB064270; BAB79695.1; -.
DR      EMBL; AF013171; AAC51762.1; -.
DR      EMBL; AB037599; BAA90488.1; -.
DR      HSSP; P50591; 1DOG.
DR      Genew; HGNC:11926; TNFSF11.
DR      MIM; 602642; -.
DR      GO; GO:0005576; C:extracellular; NAS.
DR      GO; GO:0005887; C:integral to plasma membrane; NAS.
DR      GO; GO:0005164; F:tumor necrosis factor receptor binding; NAS.
DR      GO; GO:0006955; P:immune response; NAS.
DR      GO; GO:0030316; P:osteoclast differentiation; NAS.
DR      InterPro; IPR006052; TNF_family.
DR      InterPro; IPR008983; TNF_like.
DR      InterPro; IPR003636; TNF_subf.
DR      Pfam; PF00229; TNF; 1.
DR      ProDom; PD002012; TNF_subf; 1.
DR      SMART; SM00207; TNF; 1.
DR      PROSITE; PS00251; TNF_1; FALSE_NEG.
DR      PROSITE; PS50049; TNF_2; 1.
KW      Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
KW      Signal-anchor; Alternative splicing.
FT      CHAIN      1      317      TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                                     MEMBER 11, MEMBRANE FORM.
FT      CHAIN      140     317      TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                                     MEMBER 11, SOLUBLE FORM (BY SIMILARITY).
FT      DOMAIN      1      47      CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM     48      68      SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                     (POTENTIAL).
FT      DOMAIN      69     317      EXTRACELLULAR (POTENTIAL).
FT      SITE       139     140      CLEAVAGE (BY SIMILARITY).
FT      CARBOHYD    171     171      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD    198     198      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      VARSPLIC     1      47      Missing (in isoform 3).
FT                                     /FTid=VSP_006446.
FT      VARSPLIC     1      73      Missing (in isoform 2).

```

FT /FTId=VSP\_006447.  
FT CONFLICT 194 194 A -> G (IN REF. 4).  
SQ SEQUENCE 317 AA; 35478 MW; 766176446348097F CRC64;

Query Match 100.0%; Score 1685; DB 1; Length 317;  
Best Local Similarity 100.0%; Pred. No. 3.6e-138;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHPQPPAASRSMFVALLGLGLGQV 60
        |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHPQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFahlTINATDIPSGSH 180
        |||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFahlTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
        |||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHfYSINVGGFFKLRSgEEISIEVSNPSLLD 300
        |||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHfYSINVGGFFKLRSgEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
        |||
Db    301 PDQDATYFGAFKVRDID 317
```

## RESULT 2

### TN11\_MOUSE

ID TN11\_MOUSE STANDARD; PRT; 316 AA.  
AC O35235; O35306; Q9JJK8; Q9JJK9; Q9R1Y0;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator  
DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-  
DE induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast  
DE differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor)  
DE (OCIF).  
GN TNFSF11 OR RANKL OR TRANCE OR OPGL.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Hybridoma;  
RX MEDLINE=97460112; PubMed=9312132;  
RA Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,  
RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,  
RA Choi Y.;

RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family  
RT that activates c-Jun N-terminal kinase in T cells.";  
RL J. Biol. Chem. 272:25190-25194(1997).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Thymic lymphoma;  
RX MEDLINE=98032977; PubMed=9367155;  
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,  
RA Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,  
RA Galibert L.;  
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth  
RT and dendritic-cell function.";  
RL Nature 390:175-179(1997).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Bone marrow;  
RX MEDLINE=98227661; PubMed=9568710;  
RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,  
RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,  
RA Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,  
RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,  
RA Boyle W.J.;  
RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast  
RT differentiation and activation.";  
RL Cell 93:165-176(1998).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Bone marrow stroma;  
RX MEDLINE=98188248; PubMed=9520411;  
RA Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinosaki M.,  
RA Mochizuki S.-I., Tomoyasu A., Yano K., Goto M., Murakami A., Tsuda E.,  
RA Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;  
RT "Osteoclast differentiation factor is a ligand for  
RT osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical  
RT to TRANCE/RANKL.";  
RL Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC STRAIN=129;  
RX MEDLINE=99214075; PubMed=10196481;  
RA Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,  
RA Ueda M., Higashio K.;  
RT "Cloning and characterization of the gene encoding mouse osteoclast  
RT differentiation factor.";  
RL Gene 230:121-127(1999).  
RN [6]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
RX MEDLINE=21150053; PubMed=11250921;  
RA Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;  
RT "Determination of three isoforms of the receptor activator of nuclear  
RT factor-kappaB ligand and their differential expression in bone and  
RT thymus.";  
RL Endocrinology 142:1419-1426(2001).  
RN [7]  
RP SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION.  
RX MEDLINE=99240759; PubMed=10224132;  
RA Lum L., Wong B.R., Josien R., Becherer J.D., Erdjument-Bromage H.,

RA Schloendorff J., Tempst P., Choi Y., Blobel C.P.;  
 RT "Evidence for a role of a tumor necrosis factor-alpha  
 RT (TNF-alpha)-converting enzyme-like protease in shedding of TRANCE, a  
 RT TNF family member involved in osteoclastogenesis and dendritic cell  
 RT survival.";  
 RL J. Biol. Chem. 274:13613-13618(1999).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316.  
 RX MEDLINE=21464816; PubMed=11581298;  
 RA Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.;  
 RT "Crystal structure of the TRANCE/RANKL cytokine reveals determinants  
 RT of receptor-ligand specificity.";  
 RL J. Clin. Invest. 108:971-979(2001).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-316.  
 RX MEDLINE=21839021; PubMed=11733492;  
 RA Ito S., Wakabayashi K., Ubukata O., Hayashi S., Okada F., Hata T.;  
 RT "Crystal structure of the extracellular domain of mouse RANK ligand at  
 RT 2.2-A resolution.";  
 RL J. Biol. Chem. 277:6631-6636(2002).  
 CC -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to  
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.  
 CC Augments the ability of dendritic cells to stimulate naive T-cell  
 CC proliferation. May be an important regulator of interactions  
 CC between T cells and dendritic cells and may play a role in the  
 CC regulation of the T cell-dependent immune response. May also play  
 CC an important role in enhanced bone-resorption in humoral  
 CC hypercalcemia of malignancy.  
 CC -!- SUBUNIT: Homotrimer.  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted  
 CC (isoforms 1 and 2); Cytoplasmic (isoform 3).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=1;  
 CC IsoId=O35235-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=O35235-2; Sequence=VSP\_006449;  
 CC Name=3;  
 CC IsoId=O35235-3; Sequence=VSP\_006448;  
 CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THYMUS AND LYMPH NODES BUT  
 CC NOT IN NONLYMPHOID TISSUES AND IS ABUNDANTLY EXPRESSED IN T CELLS  
 CC BUT NOT IN B CELLS. A HIGH LEVEL EXPRESSION IS ALSO SEEN IN THE  
 CC TRABECULAR BONE AND LUNG.  
 CC -!- PTM: N-glycosylated.  
 CC -!- PTM: The soluble form of isoform 1 derives from the membrane form  
 CC by proteolytic processing. The cleavage may be catalyzed by  
 CC ADAM17. A further shorter soluble form was observed.  
 CC -!- DISEASE: Deficiency in TNFSF11 results in failure to form lobulo-  
 CC alveolar mammary structures during pregnancy, resulting in death  
 CC of newborns. Trance-deficient mice show severe osteopetrosis, with  
 CC no osteoclasts, marrow spaces, or tooth eruption, and exhibit  
 CC profound growth retardation at several skeletal sites, including  
 CC the limbs, skull, and vertebrae and have marked chondrodysplasia,  
 CC with thick, irregular growth plates and a relative increase in  
 CC hypertrophic chondrocytes.  
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.  
 CC -----

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 CC -----

DR EMBL; AF013170; AAC71061.1; -.  
 DR EMBL; AF019048; AAB86812.1; -.  
 DR EMBL; AF053713; AAC40113.1; -.  
 DR EMBL; AB008426; BAA25425.1; -.  
 DR EMBL; AB022039; BAA36970.1; -.  
 DR EMBL; AB022036; BAA36970.1; JOINED.  
 DR EMBL; AB022037; BAA36970.1; JOINED.  
 DR EMBL; AB022038; BAA36970.1; JOINED.  
 DR EMBL; AB032771; BAA97257.1; -.  
 DR EMBL; AB032772; BAA97258.1; -.  
 DR EMBL; AB036798; BAA97259.1; -.  
 DR PDB; 1JTZ; 28-JAN-03.  
 DR PDB; 1IQA; 14-JAN-03.  
 DR MGD; MGI:1100089; Tnfsf11.  
 DR GO; GO:0009887; P:organogenesis; IMP.  
 DR GO; GO:0001503; P:ossification; IMP.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; FALSE\_NEG.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 KW Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;  
 KW Signal-anchor; 3D-structure; Alternative splicing.  
 FT CHAIN 1 316 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 FT MEMBER 11, MEMBRANE FORM.  
 FT CHAIN 139 316 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 FT MEMBER 11, SOLUBLE FORM.  
 FT DOMAIN 1 48 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 49 69 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT (POTENTIAL).  
 FT DOMAIN 70 316 EXTRACELLULAR (POTENTIAL).  
 FT SITE 138 139 CLEAVAGE.  
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 1 117 Missing (in isoform 3).  
 FT /FTid=VSP\_006448.  
 FT VARSPLIC 14 44 SSEEMGSGPGVPHEGPHLPAPSAPAPAPPPA -> TP (in  
 FT isoform 2).  
 FT /FTid=VSP\_006449.  
 FT CONFLICT 99 99 G -> D (IN REF. 2).  
 FT CONFLICT 141 143 MISSING (IN REF. 5).  
 FT STRAND 164 169  
 FT TURN 171 172  
 FT STRAND 181 182  
 FT STRAND 186 187  
 FT TURN 191 192



FT	STRAND	194	196
FT	STRAND	198	201
FT	TURN	202	203
FT	STRAND	204	207
FT	STRAND	211	224
FT	HELIX	225	227
FT	STRAND	234	245

Query Match 84.1%; Score 1417.5; DB 1; Length 316;  
 Best Local Similarity 84.3%; Pred. No. 4.7e-115;  
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

Qy	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPAPHPQPPAASRSMFVALLGLGLGQ	59
Db	1	MRRASRDYGKYLRSSSEEMGSGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ	60
Qy	60	VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI	119
		:	
Db	61	VVCSIALFLYFRAQMDPNRISESTHCFYRILRLHENAGLQDSTLESED--LPDSCRRM	118
Qy	120	KQAFQGAQVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFahlTINATDIPSGS	179
Db	119	KQAFQGAQVQKELQHIVGQRFSGAPAMMEGSWLDVAQRGKPEAQPFahlTINAASIPSGS	178
Qy	180	HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLM	239
		:	
Db	179	HKVTLSSWYHDRGWAKISNMTLSNGKLVRNQDGFYLYANICFRHHETSGSVPTDYLQLM	238
Qy	240	VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEIEISIEVSNPSSL	299
Db	239	VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLAGEEISIQVSNPSSL	298
Qy	300	DPDQDATYFGAFKVRDID	317
Db	299	DPDQDATYFGAFKVQDID	316

# RESULT 3

TN11\_RAT

ID TN11\_RAT STANDARD; PRT; 318 AA.  
 AC Q9ESE2; Q91ZI9;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator  
 DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-  
 DE induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast  
 DE differentiation factor) (ODF).  
 GN TNFSF11 OR RANKL OR TRANCE OR OPGL.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Tibial bone;  
 RX MEDLINE=20540945; PubMed=11092398;

RA Xu J.K., Tan J.K., Huang L., Gao X.H., Laird R., Liu D., Wysocki S.,  
 RA Zheng M.H.;  
 RT "Cloning, sequence and functional characterization of the rat  
 RT homologue of receptor activator of NF-kB ligand.";  
 RL J. Bone Miner. Res. 15:2178-2186(2000).  
 RN [2]  
 RP SEQUENCE OF 266-318 FROM N.A.  
 RC STRAIN=Fischer 344;  
 RX MEDLINE=21662371; PubMed=11804028;  
 RA Odgren P.R., Kim N., van Wesenbeeck L., MacKay C., Mason-Savas A.,  
 RA Safadi F.F., Popoff S.N., Lengner C., van-Hul W., Choi Y.,  
 RA Marks S.C. Jr.;  
 RT "Evidence that the rat osteopetrotic mutation toothless (tl) is not in  
 RT the TNFSF11 (TRANCE, RANKL, ODF, OPGL) gene.";  
 RL Int. J. Dev. Biol. 45:853-859(2001).  
 CC -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to  
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.  
 CC Augments the ability of dendritic cells to stimulate naive T-cell  
 CC proliferation. May be an important regulator of interactions  
 CC between T cells and dendritic cells and may play a role in the  
 CC regulation of the T cell-dependent immune response. May also play  
 CC an important role in enhanced bone-resorption in humoral  
 CC hypercalcemia of malignancy.  
 CC -!- SUBUNIT: Homotrimer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By  
 CC similarity).  
 CC -!- TISSUE SPECIFICITY: Highly expressed in thymus and bone tissues.  
 CC -!- PTM: The soluble form derives from the membrane form by  
 CC proteolytic processing (By similarity).  
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AF187319; AAG17031.1; -.  
 DR EMBL; AF425669; AAL23963.1; -.  
 DR HSSP; P50591; 1DOG.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; FALSE\_NEG.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 KW Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;  
 KW Signal-anchor.  
 FT CHAIN 1 318 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 FT MEMBER 11, MEMBRANE FORM.  
 FT CHAIN 141 318 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 FT MEMBER 11, SOLUBLE FORM.  
 FT DOMAIN 1 47 CYTOPLASMIC (POTENTIAL).

FT	TRANSMEM	48	68	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT				(POTENTIAL).
FT	DOMAIN	69	318	EXTRACELLULAR (POTENTIAL).
FT	SITE	140	141	CLEAVAGE (BY SIMILARITY).
FT	CARBOHYD	199	199	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	264	264	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	317	317	I -> M (IN REF. 2).
SQ	SEQUENCE	318 AA;	35370 MW;	4B87A4D706AD098F CRC64;

QY	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPAPAPHQPPAASRSMFVALLGLGLGQ	59
Db	1	MRRANRDYGYKYLRGSEEMGSCPGVPHEGPLHPAPSAPAPAPPPAASRFMFLALLGLGLGQ	60
QY	60	VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI	119
Db	61	VVCSIALFLYFRAQMDPNRISEDSTRCFYRILRLRENTGLQDSTLESEDTEALPDSCRRI	120
QY	120	KQAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPF AHLTINATDIPSGS	179
Db	121	KQAFQGA VQRELQHIVG PQRFS GVPAMMEG SWLDVARRGKPEAQPF AHLTINAADIPSGS	180
QY	180	HKVSLSSWYHDRGWAKISNM TFSNGK LIVNQDGFYYLYANICFRHHETSGDLATEYLQLM	239
Db	181	HKVSLSSWYHDRGWAKISNM TSLNGK LRVNQDGFYYLYANICFRHHETSGSV PADYLQLM	240
QY	240	VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLL	299
Db	241	VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKL RAGEEISVQVSNPSLL	300
QY	300	DPDQDATYFGAFKVRDID	317
Db	301	DPDQDATYFGAFKVODID	318

#### RESULT 4

```

ID      TN10_HUMAN          STANDARD;          PRT;    281 AA.
AC      P50591;
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Tumor necrosis factor ligand superfamily member 10 (TNF-related
DE      apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).
GN      TNFSF10 OR TRAIL OR APO2L.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=96111955; PubMed=8777713;
RA      Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
RA      Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.

```

RA Goodwin R.G.;  
 RT "Identification and characterization of a new member of the TNF  
 RT family that induces apoptosis.";  
 RL Immunity 3:673-682(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=96278649; PubMed=8663110;  
 RA Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A.,  
 RA Ashkenazi A.;  
 RT "Induction of apoptosis by Apo-2 ligand, a new member of the tumor  
 RT necrosis factor cytokine family.";  
 RL J. Biol. Chem. 271:12687-12690(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.  
 RX MEDLINE=20017054; PubMed=10549288;  
 RA Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M.,  
 RA Kelley R.F., Ashkenazi A., de Vos A.M.;  
 RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a  
 RT complex with death receptor 5.";  
 RL Mol. Cell 4:563-571(1999).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.  
 RX PubMed=10542098;  
 RA Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,  
 RA Jones E.Y., Screaton G.R.;  
 RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring  
 RT specificity in apoptotic initiation.";  
 RL Nat. Struct. Biol. 6:1048-1053(1999).  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.  
 RX MEDLINE=99413670; PubMed=10485660;  
 RA Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,

RA Sung Y.C., Oh B.-H.;  
 RT "2.8 A resolution crystal structure of human TRAIL, a cytokine with  
 RT selective antitumor activity.";  
 RL Immunity 11:253-261(1999).  
 CC -!- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,  
 CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and  
 CC possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity  
 CC may be modulated by binding to the decoy receptors  
 CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot  
 CC induce apoptosis.  
 CC -!- COFACTOR: Binds 1 zinc ion and one anionic solvent molecule per  
 CC trimer.  
 CC -!- SUBUNIT: Homotrimer.  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).  
 CC -!- TISSUE SPECIFICITY: WIDESPREAD; MOST PREDOMINANT IN SPLEEN, LUNG  
 CC AND PROSTATE.  
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.  
 CC -----  
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 CC -----  
 DR EMBL; U37518; AAC50332.1; -.  
 DR EMBL; U57059; AAB01233.1; -.  
 DR EMBL; BC032722; AAH32722.1; -.  
 DR PDB; 1D0G; 22-OCT-99.  
 DR PDB; 1D4V; 01-NOV-99.  
 DR PDB; 1D2Q; 11-FEB-00.  
 DR PDB; 1DG6; 26-SEP-01.  
 DR Genew; HGNC:11925; TNFSF10.  
 DR MIM; 603598; -.  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0005625; C:soluble fraction; TAS.  
 DR GO; GO:0005102; F:receptor binding; TAS.  
 DR GO; GO:0007267; P:cell-cell signaling; TAS.  
 DR GO; GO:0006917; P:induction of apoptosis; TAS.  
 DR GO; GO:0007165; P:signal transduction; TAS.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 KW Cytokine; Apoptosis; Transmembrane; Signal-anchor; Metal-binding;  
 KW Zinc; 3D-structure.  
 FT DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT (POTENTIAL).  
 FT DOMAIN 39 281 EXTRACELLULAR (POTENTIAL).  
 FT METAL 230 230 ZINC.  
 FT STRAND 123 127

```

FT    TURN          130    131
FT    TURN          137    139
FT    STRAND        149    150
FT    STRAND        163    165
FT    STRAND        167    170
FT    TURN          171    172
FT    STRAND        173    176
FT    STRAND        180    193
FT    STRAND        205    213
FT    STRAND        220    228
FT    STRAND        237    250
FT    TURN          252    253
FT    STRAND        255    260
FT    HELIX         263    265
FT    STRAND        266    267
FT    TURN          270    272
FT    STRAND        274    281
SQ    SEQUENCE      281 AA; 32509 MW; DDAAAF78DAAB2F6D CRC64;

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Query Match          14.9%; Score 251.5; DB 1; Length 281;
Best Local Similarity 24.1%; Pred. No. 2.3e-14;
Matches 71; Conservative 61; Mismatches 117; Indels 45; Gaps 10;

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Qy      42 PAASRSMFVALLGLGLGQVCSVALFFYFRAQMD--PNRISEDGTHCIYRILRLHENADF 99
      |:  ::  :  ::  |  |  :  |  :  ||  ::  :  :  |  :  |  |  |  |  |  :
Db      10 PSLGQTCVLIVIFTVLLQSLCVAFTYVYFTNELKQMMDKYSKSGIACF-----LKED--- 61

Qy     100 QDTTLESQDTKLIPDSCRRIKQAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSK 159
      | :  :  |  :  :  |  :  |  :  :  |  :  :  |  :  :  :  :  :  :  :
Db      62 -DSYWDPNDEESMNSPCWQV KW-----QLRQLVRKMILRTSEETI-----STVQEKQ 107

Qy     160 LEAQPF-----AHLT-----INATDIPSGSHKVSL----SSWYHDR-GWAKISNM 199
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db     108 QNISPLVRERGPQRVA AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSF LSNL 167

Qy     200 TFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEY LQLMVYVTKTSIKIPSSHTLMKGG 259
      || :  ::  :  ||  ||  :  :  ||  |  :  :  |  :  :  |  :  :  |  ||
Db     168 HLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMKSA 226

Qy     260 STKYWSGNSEFHFYSINVG GFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKV 313
      ||  ::  :  ||  ||  |  :  :  :  |  :  :  |  |  :  :  ||  ||  |
Db     227 RNSCWSKDAEYGLYSIYQG GFI FELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280

```

# RESULT 5

TN10\_MOUSE

ID TN10\_MOUSE STANDARD; PRT; 291 AA.

AC P50592;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Tumor necrosis factor ligand superfamily member 10 (TNF-related  
apoptosis inducing ligand) (TRAIL protein).

GN TNFSF10 OR TRAIL.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96111955; PubMed=8777713;
RA   Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
RA   Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
RA   Goodwin R.G.;
RT   "Identification and characterization of a new member of the TNF
RT   family that induces apoptosis.";
RL   Immunity 3:673-682(1995).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
CC   TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
CC   possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity
CC   may be modulated by binding to the decoy receptors
CC   TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot
CC   induce apoptosis.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: WIDESPREAD.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   -----
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CC   or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL; U37522; AAC52345.1; -.
DR   HSSP; P50591; 1D0G.
DR   MGD; MGI:107414; Tnfsf10.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR008983; TNF_like.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Transmembrane; Signal-anchor; Apoptosis.
FT   DOMAIN          1      17      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM        18      38      SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                     (POTENTIAL).
FT   DOMAIN          39     291     EXTRACELLULAR (POTENTIAL).
FT   CARBOHYD        52      52      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE        291 AA;  33477 MW;  3FEACAB9F0D7D802 CRC64;

Query Match          14.7%;  Score 248;  DB 1;  Length 291;
Best Local Similarity 25.4%;  Pred. No. 4.9e-14;
Matches    79;  Conservative    52;  Mismatches 100;  Indels    80;  Gaps    13;

Qy      46 RSMFVALLGLG-LGQVVCVALFFYFRAQMD--PNRISEDGTHCIYRILRLHENADFQDT 102
      | | : : : | | | : | | : | : | | : : | | | :
Db      17 RMMVICIVLLQVLLQAVSVAVTYMYFTNEMKQLQDNYSKIGLACFSK-----TDEDFWDS 71

Qy      103 TLESQDTKLIPDSCRIK-----QAFQ-----GAVOKEL 131

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      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db      72 T----DGEILNRPC LQVKRQLYQLIEEVTLR T FQDTISTVPEKQLSTPPLPRGGRPQKVA 127
Qy      132 QHIVGSQH IRAEKAMVDG SWLDLAKRSKLEA QPFAHLTINATDIPSGSHKVSLS SWYHDR 191
      || |   | : | : :   : : |   |   |   |   |   |   |   |   |   |
Db      128 AHITGITR-RSNSALI-----PISKDGKTLGQ-----KIESWESSR 162
Qy      192 -GWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYL-----QLMVYV 242
      | : : : : | || : : : | : | || : :   || |   |   | : : :   || : | :
Db      163 KGHSFLNHVLF R NGELVIEQEGLYIYSQTYFRFQEAED--ASKMVSKDKV R TKQLVQYI 220
Qy      243 TKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLDPD 302
      | :   |   |||   || : : : | || | | : | :   : | : | | : | |
Db      221 YKYT-SYPDP I VLMKSARNSCWSRDAEYGLYSIYQGGLFELKKNDRI FVSVTNEHILMDLD 279
Qy      303 QDATYFGAFKV 313
      | : | : | | | :
Db      280 QEASFFGAFLI 290

```

# RESULT 6

## TNF6\_PIG

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ID      TNF6_PIG          STANDARD;          PRT;    282 AA.
AC      Q9BEA8; Q95M04; Q95N10;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Tumor necrosis factor ligand superfamily member 6 (FAS antigen
DE      ligand).
GN      TNFSF6 OR FASL.
OS      Sus scrofa (Pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX      NCBI_TaxID=9823;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21322533; PubMed=11429161;
RA      Muneta Y., Shimoji Y., Inumaru S., Mori Y.;
RT      "Molecular cloning, characterization, and expression of porcine Fas
RT      ligand (CD95 ligand).";
RL      J. Interferon Cytokine Res. 21:305-312(2001).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Guanxi bama miniature pig;
RA      Zhu N., Young Y.;
RT      "Molecular cloning and characterization of porcine Fas ligand cDNA.";
RL      Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Lymphoid;
RA      Tsuyuki S., Kono M., Bloom E.T.;
RT      "Cloning and potential utility of porcine Fas ligand: overexpression
RT      in porcine cells protects them from attack by human cytolytic cells.";
RL      Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN      [4]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Landrace x Large Yorkshire white; TISSUE=Thymocytes;

```



RX MEDLINE=21653191; PubMed=11792426;  
 RA Motegi-Ishiyama Y., Nakajima Y., Hoka S., Takagaki Y.;  
 RT "Porcine Fas-ligand gene: genomic sequence analysis and comparison  
 RT with human gene.";  
 RL Mol. Immunol. 38:581-586(2002).  
 CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that  
 CC transduces the apoptotic signal into cells. May be involved in  
 CC cytotoxic T cell mediated apoptosis and in T cell development.  
 CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of  
 CC peripheral tolerance, in the antigen-stimulated suicide of mature  
 CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3  
 CC modulates its effects (By similarity).  
 CC -!- SUBUNIT: Homotrimer (Probable).  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By  
 CC similarity).  
 CC -!- INDUCTION: By IL-18.  
 CC -!- PTM: The soluble form derives from the membrane form by  
 CC proteolytic processing (By similarity).  
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.  
 CC -----  
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 CC -----  
 DR EMBL; AB027297; BAB40919.1; -.  
 DR EMBL; AY033634; AAK56449.1; -.  
 DR EMBL; AF397407; AAK84408.1; -.  
 DR EMBL; AB069764; BAB64291.1; -.  
 DR HSSP; P01375; 4TSV.  
 DR InterPro; IPR008064; Fas\_ligand.  
 DR InterPro; IPR006053; TNF\_abc.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01681; FASLIGAND.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 KW Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.  
 FT CHAIN 1 282 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 FT MEMBER 6, MEMBRANE FORM.  
 FT CHAIN 131 282 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 FT MEMBER 6, SOLUBLE FORM (BY SIMILARITY).  
 FT DOMAIN 1 82 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 83 103 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT (POTENTIAL).  
 FT DOMAIN 104 282 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 4 70 PRO-RICH.  
 FT DOMAIN 45 56 POLY-PRO.  
 FT SITE 130 131 CLEAVAGE (BY SIMILARITY).

FT DISULFID 203 234 POTENTIAL.  
 FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 5 5 F -> L (IN REF. 4).  
 FT CONFLICT 57 57 T -> P (IN REF. 2).  
 SQ SEQUENCE 282 AA; 31756 MW; 6743DAA1145671FB CRC64;

Query Match 11.9%; Score 200; DB 1; Length 282;  
 Best Local Similarity 23.0%; Pred. No. 6.5e-10;  
 Matches 76; Conservative 42; Mismatches 90; Indels 122; Gaps 14;

QY 22 PGAPHEGPLHAPPPAPHQPPAA---SRSM-----FVA 51  
 || | | ||| | || :  
 Db 37 PGRP--GQRRPPPPPPPPPTLLPSRPLPPLPPPSLKKKRDHNAGLCLLVMMFFMVLVA 94  
 QY 52 LLGLGLGQVVCVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKL 111  
 |:|||| :| | : : | |:| : |  
 Db 95 LVGLGLG-----MFQLFHLQKE-----LTELRESASQRHT----- 124  
 QY 112 IPDSCRRIKQAFQGA VQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLT-- 169  
 : | : :| :: :|| | : ||||  
 Db 125 -----ESSLEKQIGHPNLPSEKK-----ELRKVAHLTGK 153  
 QY 170 INATDIPSGSHKVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSG 229  
 |: || | | :| : : | |::| | |::| : : || :  
 Db 154 PNSRSIP-----LEWEDTYGIALVSGVKYMKGSLVINDTGLYFVYSKVYFRGQYCN- 204  
 QY 230 DLATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKY-----WSGNSEFHFYSINVGGFFKL 283  
 : | || |: | : | ||:| | : :| : | | |  
 Db 205 ---NQPLSHKVY-TRNS-RYPQDLVLMEGKMMNYCTTGQMWARSS-----YLGAVFNL 252  
 QY 284 RSGEEISIEVSNPSLLDPDQDATYFGAFKV 313  
 | : : : || ||:: : : |:|| : :  
 Db 253 TSADHLYVNVSELSLVNFEESKTFFGLYKL 282

# RESULT 7

## TNF6\_HUMAN

ID TNF6\_HUMAN STANDARD; PRT; 281 AA.  
 AC P48023; Q9BZP9;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)  
 DE (Apoptosis antigen ligand) (APTL) (CD178 antigen).  
 GN TNFSF6 OR FASL OR APT1LG1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=95105731; PubMed=7528780;  
 RA Alderson M.;  
 RT "Fas ligand mediates activation-induced cell death in human T  
 RT lymphocytes.";

RL J. Exp. Med. 181:71-77(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=95127560; PubMed=7826947;  
 RA Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;  
 RT "Human Fas ligand: gene structure, chromosomal location and species  
 RT specificity.";  
 RL Int. Immunol. 6:1567-1574(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RA Schaetzlein C.E., Poehlmann R., Philippsen P., Eibel H.;  
 RL Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=95071350; PubMed=7980502;  
 RA Mita E., Hayashi N., Iio S., Takehara T., Hijioaka T., Kasahara A.,  
 RA Fusamoto H., Kamada T.;  
 RT "Role of Fas ligand in apoptosis induced by hepatitis C virus  
 RT infection.";  
 RL Biochem. Biophys. Res. Commun. 204:468-474(1994).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RC TISSUE=Leukocyte;  
 RA Zeytun A., Nagarkatti M., Nagarkatti P.S.;  
 RT "Isolation and characterization of a new naturally occurring variant of  
 RT human Fas ligand that is expressed only in membrane bound form.";  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA Wilkinson J.;  
 RL Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Blood;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [8]  
 RP SEQUENCE OF 1-10 FROM N.A.

RC TISSUE=Blood;  
 RA Matsumura M., Nakanishi Y., Ohba Y.;  
 RL Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.  
 RN [9]  
 RP CHARACTERIZATION, AND MUTAGENESIS OF PRO-206; TYR-218 AND PHE-275.  
 RX MEDLINE=97373583; PubMed=9228058;  
 RA Schneider P., Bodmer J.-L., Holler N., Mattmann C., Scuderi P.,  
 RA Terskikh A., Peitsch M.C., Tschopp J.;  
 RT "Characterization of Fas (Apo-1, CD95)-Fas ligand interaction.";  
 RL J. Biol. Chem. 272:18827-18833(1997).  
 RN [10]  
 RP PROCESSING.  
 RX MEDLINE=98087475; PubMed=9427603;  
 RA Tanaka M., Itai T., Adachi M., Nagata S.;  
 RT "Downregulation of Fas ligand by shedding.";  
 RL Nat. Med. 4:31-36(1998).  
 CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that  
 CC transduces the apoptotic signal into cells. May be involved in  
 CC cytotoxic T cell mediated apoptosis and in T cell development.  
 CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of  
 CC peripheral tolerance, in the antigen-stimulated suicide of mature  
 CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3  
 CC modulates its effects.  
 CC -!- SUBUNIT: Homotrimer (Probable).  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein. May be released  
 CC into the extracellular fluid, probably by cleavage from the cell  
 CC surface.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=P48023-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=P48023-2; Sequence=VSP\_006443, VSP\_006444;  
 CC -!- PTM: N-glycosylated.  
 CC -!- PTM: The soluble form derives from the membrane form by  
 CC proteolytic processing.  
 CC -!- DISEASE: Defects in TNFSF6 are a cause of autoimmune  
 CC lymphoproliferative syndrome (ALPS) [MIM:601859]; also known as  
 CC Canale-Smith syndrome (CSS). ALPS is a childhood syndrome  
 CC involving hemolytic anemia and thrombocytopenia with massive  
 CC lymphadenopathy and splenomegaly.  
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.  
 CC -!- DATABASE: NAME=PROW; NOTE=PROW 2:59-69(2001);  
 CC WWW="[http://www.ncbi.nlm.nih.gov/prow/guide/333879674\\_g.htm](http://www.ncbi.nlm.nih.gov/prow/guide/333879674_g.htm)".  
 CC -----  
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 CC -----  
 DR EMBL; X89102; CAA61474.1; -.  
 DR EMBL; U08137; AAC50071.1; -.  
 DR EMBL; U11821; AAC50124.1; -.  
 DR EMBL; D38122; BAA07320.1; -.

DR EMBL; AF288573; AAG60017.1; -.  
 DR EMBL; Z96050; CAB09424.1; -.  
 DR EMBL; BC017502; AAH17502.1; -.  
 DR EMBL; AB013303; BAA32542.1; -.  
 DR PIR; I38707; I38707.  
 DR HSSP; P01375; 1TNF.  
 DR Genew; HGNC:11936; TNFSF6.  
 DR MIM; 134638; -.  
 DR MIM; 601859; -.  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0005102; F:receptor binding; TAS.  
 DR GO; GO:0007267; P:cell-cell signaling; TAS.  
 DR GO; GO:0006917; P:induction of apoptosis; TAS.  
 DR GO; GO:0007165; P:signal transduction; TAS.  
 DR InterPro; IPR008064; Fas\_ligand.  
 DR InterPro; IPR006053; TNF\_abc.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01681; FASLIGAND.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 KW Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor;  
 KW Alternative splicing; Antigen.  
 FT CHAIN 1 281 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 FT MEMBER 6, MEMBRANE FORM.  
 FT CHAIN 130 281 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 FT MEMBER 6, SOLUBLE FORM.  
 FT DOMAIN 1 80 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 81 102 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT (POTENTIAL).  
 FT DOMAIN 103 281 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 4 70 PRO-RICH.  
 FT DOMAIN 45 65 POLY-PRO.  
 FT SITE 129 130 CLEAVAGE.  
 FT DISULFID 202 233 POTENTIAL.  
 FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 117 127 STSQMHTASSL -> ATPVHPLKKRS (in isoform  
 FT 2).  
 FT /FTId=VSP\_006443.  
 FT VARSPLIC 128 281 Missing (in isoform 2).  
 FT /FTId=VSP\_006444.  
 FT MUTAGEN 206 206 P->D,F,R: LOWERS BINDING TO TNFRSF6 AND  
 FT REDUCES CYTOTOXICITY MORE THAN 100-FOLD.  
 FT MUTAGEN 218 218 Y->F,R: LOWERS BINDING TO TNFRSF6 AND  
 FT ABOLISHES CYTOTOXICITY.  
 FT MUTAGEN 275 275 F->L: ABOLISHES BINDING TO TNFRSF6 AND  
 FT CYTOTOXICITY.  
 SQ SEQUENCE 281 AA; 31485 MW; A8A6EB358246E9BB CRC64;

Query Match 11.2%; Score 189; DB 1; Length 281;

Best Local Similarity 21.7%; Pred. No. 5.8e-09;  
Matches 69; Conservative 43; Mismatches 98; Indels 108; Gaps 11;

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QY      22 PGAPHEGPLHAPPPAP----HQPPAASRS-----MFVALLGLGLGQVVCS 63
      | |  | |  | | | |  | |  |  : | | : | | | |
Db      46 PPPPPPPPLPPPPPPPLPPLPLPPLKKRGNHSTGLCLLMFFMVLVALVGLGLG----- 100

QY      64 VALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAF 123
      : | | |  | |  | | : : : | :
Db     101 --MFQLFHLQ-----KELAE LRESTSQMHTA----- 124

QY     124 QGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLT--INATDIPSGSHK 181
      : : | : : |  | | : | | | | | : : |
Db     125 -SSLEKQIGH-----PSPPPPEKKELRKVAHLTGKSNRSRSM----- 159

QY     182 VSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEY LQIMVY 241
      | |  | : | : : | | : : | | : : : | | : |
Db     160 ---LEWEDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQSCNN-----LPLSHK 210

QY     242 VTKTSIKIPSSHTLMKGGSTKY-----WSGNSEFHFYSINVGFFFKLRSGEEISIEVSN 295
      | : | | : | : | | : : | : | | | : : : | |
Db     211 VYMRNSKYPQDLVMMEGKMMSYCTTGQMWARSS-----YLGAVFNLT SADHLYVNVSE 263

QY     296 PSLLDPDQDATYFGAFKV 313
      | | : : : | : | | : |
Db     264 LSLVNFEESQTFFGLYKL 281

```

#### RESULT 8

##### TNF6\_MACMU

```

ID   TNF6_MACMU          STANDARD;          PRT;   280 AA.
AC   Q9MYL6; Q9BDM5;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
DE   (CD95L protein).
GN   TNFSF6 OR FASL OR CD95L.
OS   Macaca mulatta (Rhesus macaque),
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
OS   Macaca nemestrina (Pig-tailed macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544, 9541, 9545;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=M.mulatta; TISSUE=Lymphocytes;
RX   MEDLINE=21383618; PubMed=11491535;
RA   Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA   Weiss W.R., Ansari A.A.;
RT   "Cloning, sequencing, and homology analysis of nonhuman primate
RT   Fas/Fas-ligand and co-stimulatory molecules.";
RL   Immunogenetics 53:315-328(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;

```

RA Kirii Y., Inoue T., Yoshino K.;  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.  
 CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that  
 CC transduces the apoptotic signal into cells. May be involved in  
 CC cytotoxic T cell mediated apoptosis and in T cell development.  
 CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of  
 CC peripheral tolerance, in the antigen-stimulated suicide of mature  
 CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3  
 CC modulates its effects (By similarity).  
 CC -!- SUBUNIT: Homotrimer (Potential).  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By  
 CC similarity).  
 CC -!- PTM: The soluble form derives from the membrane form by  
 CC proteolytic processing (By similarity).  
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AF344856; AAK37539.1; -.  
 DR EMBL; AB035138; BAA90294.1; -.  
 DR EMBL; AB035139; BAA90295.1; -.  
 DR EMBL; AB035140; BAA90296.1; -.  
 DR HSSP; P01375; 4TSV.  
 DR InterPro; IPR008064; Fas\_ligand.  
 DR InterPro; IPR006053; TNF\_abc.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01681; FASLIGAND.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 KW Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.  
 FT CHAIN 1 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 FT MEMBER 6, MEMBRANE FORM.  
 FT CHAIN 129 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 FT MEMBER 6, SOLUBLE FORM (BY SIMILARITY).  
 FT DOMAIN 1 80 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 81 101 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT (POTENTIAL).  
 FT DOMAIN 102 280 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 4 69 PRO-RICH.  
 FT DOMAIN 45 64 POLY-PRO.  
 FT SITE 128 129 CLEAVAGE (BY SIMILARITY).  
 FT DISULFID 201 232 POTENTIAL.  
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CONFLICT 60 60 S -> P (IN REF. 1).  
SQ SEQUENCE 280 AA; 31367 MW; F0B284D61A132EB4 CRC64;

Query Match 11.0%; Score 186; DB 1; Length 280;  
Best Local Similarity 22.1%; Pred. No. 1e-08;  
Matches 69; Conservative 44; Mismatches 103; Indels 96; Gaps 11;

```
Qy      22 PGAPHEGPHLHAPPPAP----HQPPAASRS-----MFVALLGLGLGQVVCS 63
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      45 P P P P P P P P L P P P P P S P L P P L P L P P L K K R G N H S T G L C L L V M F F M V L V A L V G L G L G ---- 99

Qy      64 VALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAF 123
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     100 --MFQLFHLQ-----KELAE LRESTSQKHTA----- 123

Qy     124 QGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLT--INATDIPSGSHK 181
      : : | : | | | | | | | | | | | | | | | | | | | | | |
Db     124 -SSLEKQIGH-----PSPPEKKEQRKVAHLTGKPNRSRSM----- 158

Qy     182 VSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQMVY 241
      | | | | | : | : : | | : : | | : : | | : : | | | | | |
Db     159 ---LEWEDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFR-----GQSCTN-LPLSHK 209

Qy     242 VTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEIEISIEVSNPSLLDP 301
      | : | | : | : | | : : : | : | | | : : : | | | : |
Db     210 VYMRNSKYPQDLVMMEGKMMSYCT-TGQMWAHSSYLGAVERNLTADHLYVNVSELSLVNF 268

Qy     302 DQDATYFGAFKV 313
      : : | : | | : | :
Db     269 EESQTFFGLYKL 280
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#### RESULT 9

##### TNF6\_MOUSE

ID TNF6\_MOUSE STANDARD; PRT; 279 AA.  
AC P41047; Q61217; Q9R1F2;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen  
DE ligand).  
GN TNFSF6 OR FASL OR APT1LG1 OR GLD.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM FASL).  
RX MEDLINE=94185175; PubMed=7511063;  
RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,  
RA Suda T., Nagata S.;  
RT "Generalized lymphoproliferative disease in mice, caused by a point  
RT mutation in the Fas ligand."  
RL Cell 76:969-976(1994).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.  
RC STRAIN=C57BL/6;



RX MEDLINE=95388076; PubMed=7544870;  
 RA Peitsch M.J., Tschopp J.J.;  
 RT "Comparative molecular modelling of the Fas-ligand and other members  
 RT of the TNF family.";  
 RL Mol. Immunol. 32:761-772(1995).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM FASL).  
 RX MEDLINE=95196085; PubMed=7889405;  
 RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,  
 RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;  
 RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a  
 RT TNF family gene cluster.";  
 RL Immunity 1:131-136(1994).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM FASL).  
 RC STRAIN=BALB/c;  
 RA Fenner M.H., Shioda T., Isselbacher K.J.;  
 RT "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in  
 RT two amino acids.";  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM FASLS).  
 RC STRAIN=C3H; TISSUE=Spleen;  
 RX MEDLINE=20021694; PubMed=10552956;  
 RA Ayroldi E., D'Adamio F., Zollo O., Agostini M., Moraca R.,  
 RA Cannarile L., Migliorati G., Delfino D.V., Riccardi C.;  
 RT "Cloning and expression of a short Fas ligand: A new alternatively  
 RT spliced product of the mouse Fas ligand gene.";  
 RL Blood 94:3456-3467(1999).  
 RN [6]  
 RP CHARACTERIZATION OF VARIANT GLD.  
 RX MEDLINE=96091792; PubMed=7495745;  
 RA Hahne M., Peitsch M.C., Irmeler M., Schroeter M., Lowin B.,  
 RA Rousseau M., Bron C., Renno T., French L., Tschopp J.;  
 RT "Characterization of the non-functional Fas ligand of gld mice.";  
 RL Int. Immunol. 7:1381-1386(1995).  
 RN [7]  
 RP VARIANTS ALA-184 AND GLY-218.  
 RC STRAIN=C57BL/6, C3H, MRL, SJL, NOD, NZB, NZW, BALB/c, DBA/1, and  
 RC DBA/2;  
 RX MEDLINE=97268671; PubMed=9108079;  
 RA Kayagaki N., Yamaguchi N., Nagao F., Matsuo S., Maeda H., Okumura K.,  
 RA Yagita H.;  
 RT "Polymorphism of murine Fas ligand that affects the biological  
 RT activity.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:3914-3919(1997).  
 CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that  
 CC transduces the apoptotic signal into cells. May be involved in  
 CC cytotoxic T cell mediated apoptosis and in T cell development.  
 CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of  
 CC peripheral tolerance, in the antigen-stimulated suicide of mature  
 CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3  
 CC modulates its effects (By similarity).  
 CC -!- SUBUNIT: Homotrimer (Probable).  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein (isoform FASL);  
 CC Secreted (isoforms FASL and FASLS).  
 CC -!- ALTERNATIVE PRODUCTS:

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CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=FasL;
CC      IsoId=P41047-1; Sequence=Displayed;
CC      Name=FasLS;
CC      IsoId=P41047-2; Sequence=VSP_006445;
CC      -!- PTM: The soluble form derives from the membrane form by
CC      proteolytic processing (By similarity).
CC      -!- DISEASE: A deficiency in this protein is the cause of generalized
CC      lymphoproliferation disease phenotype (gld). Gld mice present
CC      lymphadenopathy and autoantibody production. The phenotype is
CC      recessively inherited.
CC      -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC      -----
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CC      -----
DR      EMBL; U06948; AAA17800.1; -.
DR      EMBL; U10984; AAA19778.1; -.
DR      EMBL; S76752; AAB33780.1; -.
DR      EMBL; U58995; AAB02915.1; -.
DR      EMBL; AF119335; AAD52106.1; -.
DR      PIR; A53062; A53062.
DR      HSSP; P01375; 4TSV.
DR      MGD; MGI:99255; Tnfsf6.
DR      InterPro; IPR008064; Fas_ligand.
DR      InterPro; IPR006053; TNF_abc.
DR      InterPro; IPR006052; TNF_family.
DR      InterPro; IPR008983; TNF_like.
DR      InterPro; IPR003636; TNF_subf.
DR      Pfam; PF00229; TNF; 1.
DR      PRINTS; PR01681; FASLIGAND.
DR      PRINTS; PR01234; TNECROSISFCT.
DR      ProDom; PD002012; TNF_subf; 1.
DR      SMART; SM00207; TNF; 1.
DR      PROSITE; PS00251; TNF_1; 1.
DR      PROSITE; PS50049; TNF_2; 1.
KW      Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor;
KW      Disease mutation; Polymorphism; Alternative splicing.
FT      CHAIN      1      279      TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                                     MEMBER 6, MEMBRANE FORM.
FT      CHAIN      128     279      TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                                     MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
FT      DOMAIN      1      78      CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM     79     100      SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                     (POTENTIAL).
FT      DOMAIN     101     279      EXTRACELLULAR (POTENTIAL).
FT      DOMAIN      4      69      PRO-RICH.
FT      DOMAIN     45      51      POLY-PRO.
FT      SITE       127     128      CLEAVAGE (BY SIMILARITY).
FT      DISULFID    200     231      POTENTIAL.
FT      CARBOHYD    117     117      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD    182     182      N-LINKED (GLCNAC. . .) (POTENTIAL).

```

FT	CARBOHYD	248	248	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	258	258	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	1	210	Missing (in isoform FasLS).
FT				/FTId=VSP_006445.
FT	VARIANT	184	184	T -> A (IN STRAINS BALB/C AND DBA;
FT				ENHANCES CYTOTOXICITY).
FT	VARIANT	218	218	E -> G (IN STRAINS BALB/C AND DBA;
FT				ENHANCES CYTOTOXICITY).
FT	VARIANT	273	273	F -> L (IN GLD; ABOLISHES BINDING OF FASL
FT				TO ITS RECEPTOR).
SQ	SEQUENCE	279 AA;	31442 MW;	37972E2728E0A1CA CRC64;

Query Match 10.9%; Score 184.5; DB 1; Length 279;  
 Best Local Similarity 21.7%; Pred. No. 1.4e-08;  
 Matches 70; Conservative 45; Mismatches 106; Indels 101; Gaps 11;

Qy	13	RGSEEMGGGPGAPHEGPLHAPPPAPHPQ-----PAASRSMFVALLGLGL	57
		: :                 :     :	
Db	38	RGPDQRRPPPPPPVSPPLPPSQPLPLPLPLTPLKKKDHNTNLWLPVVFFMVLVALVGMGL	97
Qy	58	GQVVCVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCR	117
		:   :	
Db	98	G-----MYQLFHL-----	105
Qy	118	RIKQAFQGA VQKELQHI--VGSQHRA---EKAMVDGSWLDLAKRSKLEAQPFAHLTINA	172
		: :   : :     : :     :	
Db	106	-----QKELAE LREFTNQSLKVSSF EKQIANPS----TPSEKKEPRSV AHLTGN-	150
Qy	173	TDIPSGSHKVSLS-SWYHDRGWAKISNMFTSNGKLIVNQDGFYYLYANICFRHHETSGDL	231
		:         : :   : :     : :     : :	
Db	151	-----PHSRSIPLWEDTYGTALISGVK YKKGGLVINETGLYFVYSKVYFRGQSCN---	201
Qy	232	ATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISI	291
		:     : :       : :   : : :   :       : : :	
Db	202	-NQPLNHKVYMRNS--KYPEDLVLME EKRLNYCT-TGQIWAHSSYLGA VFNLT SADHLYV	257
Qy	292	EVSNP SLLDPDQDATYFGAFKV	313
		:     : : :   :   :	
Db	258	NISQLSLINF EESKTF FGLYKL	279

# RESULT 10

## TNF6\_CERTO

ID	TNF6_CERTO	STANDARD;	PRT;	280 AA.
AC	Q9BDN1;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)			
DE	(CD95L protein).			
GN	TNFSF6 OR FASL OR CD95L.			
OS	Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;			
OC	Cercopithecinae; Cercopithecus.			
OX	NCBI_TaxID=9531;			
RN	[1]			

RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymphocytes;  
 RX MEDLINE=21383618; PubMed=11491535;  
 RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,  
 RA Weiss W.R., Ansari A.A.;  
 RT "Cloning, sequencing, and homology analysis of nonhuman primate  
 RT Fas/Fas-ligand and co-stimulatory molecules.";  
 RL Immunogenetics 53:315-328(2001).  
 CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that  
 CC transduces the apoptotic signal into cells. May be involved in  
 CC cytotoxic T cell mediated apoptosis and in T cell development.  
 CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of  
 CC peripheral tolerance, in the antigen-stimulated suicide of mature  
 CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3  
 CC modulates its effects (By similarity).  
 CC -!- SUBUNIT: Homotrimer (Probable).  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By  
 CC similarity).  
 CC -!- PTM: The soluble form derives from the membrane form by  
 CC proteolytic processing (By similarity).  
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.  
 CC -----  
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 CC -----  
 DR EMBL; AF344847; AAK37606.1; -.  
 DR HSSP; P01375; 4TSV.  
 DR InterPro; IPR008064; Fas\_ligand.  
 DR InterPro; IPR006053; TNF\_abc.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01681; FASLIGAND.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 KW Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.  
 FT CHAIN 1 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 FT MEMBER 6, MEMBRANE FORM.  
 FT CHAIN 129 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 FT MEMBER 6, SOLUBLE FORM (BY SIMILARITY).  
 FT DOMAIN 1 80 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 81 101 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT (POTENTIAL).  
 FT DOMAIN 102 280 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 4 69 PRO-RICH.  
 FT DOMAIN 45 64 POLY-PRO.  
 FT SITE 128 129 CLEAVAGE (BY SIMILARITY).  
 FT DISULFID 201 232 POTENTIAL.

FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 280 AA; 31407 MW; 729EA60067B7D398 CRC64;

Query Match 10.8%; Score 182.5; DB 1; Length 280;  
 Best Local Similarity 22.4%; Pred. No. 2.1e-08;  
 Matches 70; Conservative 44; Mismatches 100; Indels 99; Gaps 12;

Qy 22 PGAPHEGPHLHAPPPAPHPQPP-----AASRS-----MFVALLGLGLGQVVC 62  
 | | | | | | | | | | : | : | | | | |  
 Db 46 P P P P P P P P L -- P P P P P P L P P L P L P P L K K R G N H S T G L C L L V M F F M V L V A L V G L G L G ---- 99  
 Qy 63 SVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQA 122  
 : | | | | : | | : : : | :  
 Db 100 ---MFQLFHLQ-----KELAE LRESTSQKHTA----- 123  
 Qy 123 FQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHLT--INATDIPSGSH 180  
 : : : | : : | | : | | | | : : |  
 Db 124 --SSLEKQIGH-----PSPPEKKEQRKVAHLTGKPNRSRMP---- 158  
 Qy 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQMV 240  
 | | : | : : | | : : | | : : : | | | | |  
 Db 159 ----LEWEDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFR-----GQSCTN-LPLSH 208  
 Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEIEISIEVSNPSLLD 300  
 | : | | : | : | : : | : | | : : : | | : : :  
 Db 209 KVMYMRNSKYPQDLVMMEGKMSYCT-TGQMWAHSSYLGA VFNLTSTDHLYVNVSEL SLVN 267  
 Qy 301 PDQDATYFGAFKV 313  
 : : | : | : | :  
 Db 268 FEESQTFFGLYKL 280

# RESULT 11

TNF5\_BOVIN

ID TNF5\_BOVIN STANDARD; PRT; 261 AA.

AC P51749;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (TNF-related activation protein) (TRAP) (T cell antigen GP39).

GN TNFSF5 OR CD40LG OR CD40L.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

OC Bovidae; Bovinae; Bos.

OX NCBI\_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Blood;

RX MEDLINE=96006582; PubMed=7590981;

RA Mertens B.E.L.C., Muriuki M., Gaidulis L.;

RT "Cloning of two members of the TNF-superfamily in cattle: CD40 ligand and tumor necrosis factor alpha.";

RL Immunogenetics 42:430-431(1995).

CC -!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell  
CC proliferation in the absence of co-stimulus as well as IgE  
CC production in the presence of IL-4. Involved in immunoglobulin  
CC class switching (By similarity).  
CC -!- SUBUNIT: Homotrimer (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an  
CC extracellular soluble form (By similarity).  
CC -!- PTM: The soluble form derives from the membrane form by  
CC proteolytic processing (By similarity).  
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.

-----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----

DR EMBL; Z48469; CAA88363.1; -.  
DR PIR; S53090; S53090.  
DR HSSP; P29965; 1ALY.  
DR GO; GO:0016021; C:integral to membrane; ISS.  
DR GO; GO:0005174; F:CD40 receptor binding; ISS.  
DR GO; GO:0042100; P:B-cell proliferation; ISS.  
DR GO; GO:0006954; P:inflammatory response; ISS.  
DR GO; GO:0007159; P:leukocyte cell adhesion; ISS.  
DR GO; GO:0030168; P:platelet activation; ISS.  
DR InterPro; IPR003263; TNF\_5.  
DR InterPro; IPR006052; TNF\_family.  
DR InterPro; IPR008983; TNF\_like.  
DR InterPro; IPR003636; TNF\_subf.  
DR Pfam; PF00229; TNF; 1.  
DR PRINTS; PR01702; CD40LIGAND.  
DR ProDom; PD008600; TNF\_5; 1.  
DR ProDom; PD002012; TNF\_subf; 1.  
DR SMART; SM00207; TNF; 1.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS50049; TNF\_2; 1.  
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.

FT	CHAIN	1	261	TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT				MEMBER 5, MEMBRANE FORM.
FT	CHAIN	113	261	TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT				MEMBER 5, SOLUBLE FORM (BY SIMILARITY).
FT	DOMAIN	1	22	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	23	46	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT				(POTENTIAL).
FT	DOMAIN	47	261	EXTRACELLULAR (POTENTIAL).
FT	SITE	112	113	CLEAVAGE (BY SIMILARITY).
FT	DISULFID	178	218	POTENTIAL.
FT	CARBOHYD	240	240	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	261 AA;	29242 MW;	8491FEFB30A787FD CRC64;

Query Match 10.5%; Score 176.5; DB 1; Length 261;  
Best Local Similarity 24.2%; Pred. No. 6.3e-08;  
Matches 70; Conservative 54; Mismatches 122; Indels 43; Gaps 13;

Qy 33 PPPAPHQPPAASRSMFVALLGLGL-GQVVCVVALFFYFRAQMDPNRISEDGTHCIYRIL 91  
 | | : | | : | : | | : | | : | : | : | : | : | :  
 Db 8 PPSRSVATGPPVSMKIFMYLLTVFLITQMIGSALFAVYLHRRLD--KIEDE-----R 57

Qy 92 RLHENADFQDT--TLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDG 149  
 |||: | | : | : | : | : | : | : | : | : | : | :  
 Db 58 NLHEDFVFMKTIQRCNKGEGLSLLNCEEIRSRFEDLVKDIMQ---NKEVKKKEKNFE- 112

Qy 150 SWLDLAKRSKLEAQPPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISN--MTFSNGK-L 206  
 : | | ||: | : | : | : | : | : | : | : | : | :  
 Db 113 -----MHKGDQEPQIAAHVISEAS-----SKTTSVLQW-APKGYTSLNNLVLTLENGKQL 161

Qy 207 IVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIP--SSHTLMKGGSTKYW 264  
 | : ||||: | : | : | : | : | : | : | : | : | :  
 Db 162 AVKRQGFYYIYTQVTFCNSR-----ETLSQAPFIASLCLKSPSGSERILLRAANTH-- 212

Qy 265 SGNSEFHFYSINVGGFFKLRSGEESIEVSNPSLLDPDQDATYFGAFKV 313  
 | : ||: || | : || : : | : || : | | | :  
 Db 213 SSSKPCGQQSIHLGGVFELQSGASVFVNVTDPQVSHGTGFTSFGLLKL 261

# RESULT 12

## TNF6\_RAT

ID TNF6\_RAT STANDARD; PRT; 278 AA.  
 AC P36940;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen  
 DE ligand).  
 GN TNFSF6 OR FASL OR APT1LG1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94084792; PubMed=7505205;  
 RA Suda T., Takahashi T., Golstein P., Nagata S.;  
 RT "Molecular cloning and expression of the Fas ligand, a novel member  
 RT of the tumor necrosis factor family."  
 RL Cell 75:1169-1178(1993).  
 CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that  
 CC transduces the apoptotic signal into cells. May be involved in  
 CC cytotoxic T cell mediated apoptosis and in T cell development.  
 CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of  
 CC peripheral tolerance, in the antigen-stimulated suicide of mature  
 CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3  
 CC modulates its effects (By similarity).  
 CC -!- SUBUNIT: Homotrimer (Probable).  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By  
 CC similarity).  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED SPLENOCYTES AND  
 CC THYMOCYTES. MODERATE OR WEAK EXPRESSION FOUND IN SMALL INTESTINES,  
 CC KIDNEY AND LUNG.  
 CC -!- INDUCTION: BY PMA/IONOMYCIN AND CONCAVALIN/INTERLEUKIN-2.  
 CC -!- PTM: The soluble form derives from the membrane form by

CC       proteolytic processing (By similarity).  
 CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.  
 CC   -----  
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 CC   -----  
 DR   EMBL; U03470; AAC52129.1; -.  
 DR   PIR; A49266; A49266.  
 DR   HSSP; P01375; 4TSV.  
 DR   InterPro; IPR008064; Fas\_ligand.  
 DR   InterPro; IPR006053; TNF\_abc.  
 DR   InterPro; IPR006052; TNF\_family.  
 DR   InterPro; IPR008983; TNF\_like.  
 DR   InterPro; IPR003636; TNF\_subf.  
 DR   Pfam; PF00229; TNF; 1.  
 DR   PRINTS; PR01681; FASLIGAND.  
 DR   PRINTS; PR01234; TNECROSISFCT.  
 DR   ProDom; PD002012; TNF\_subf; 1.  
 DR   SMART; SM00207; TNF; 1.  
 DR   PROSITE; PS00251; TNF\_1; 1.  
 DR   PROSITE; PS50049; TNF\_2; 1.  
 KW   Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.  
 FT   CHAIN           1       278       TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 FT                                   MEMBER 6, MEMBRANE FORM.  
 FT   CHAIN           127      278       TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 FT                                   MEMBER 6, SOLUBLE FORM (BY SIMILARITY).  
 FT   DOMAIN          1       77       CYTOPLASMIC (POTENTIAL).  
 FT   TRANSMEM       78      99       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT                                   (POTENTIAL).  
 FT   DOMAIN          100     278       EXTRACELLULAR (POTENTIAL).  
 FT   DOMAIN          4       69       PRO-RICH.  
 FT   DOMAIN          45      58       POLY-PRO.  
 FT   SITE           126     127       CLEAVAGE (BY SIMILARITY).  
 FT   DISULFID       199     230       POTENTIAL.  
 FT   CARBOHYD       116     116       N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT   CARBOHYD       247     247       N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT   CARBOHYD       257     257       N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ   SEQUENCE       278 AA;   31140 MW;   2898E18A862CEAC6 CRC64;

Query Match                   10.4%;   Score 175.5;   DB 1;   Length 278;  
 Best Local Similarity       20.3%;   Pred. No. 8.4e-08;  
 Matches   64;   Conservative   47;   Mismatches 106;   Indels   99;   Gaps   10;

Qy           21 GPGAPHEGPLHAPPPAPHPQPPAASRSM-----FVALLGLGL 57  
              |||    |   ||||:|   ||:       :               |||:|:|  
 Db           39 GPGQRRPPP--PPPPPSPLPPPSQPPPLPPLSPLKKKDNIELWLPVIFFMVLVALVGMGL 96  
  
 Qy           58 GQVVC SVALFFYFRAQMDPNRI SEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCR 117  
              |       :: |   | :   : |   | : | :       :   | |:: : :  
 Db           97 G-----MYQLFHLQKELAE LREFTNHSL-RVSSFEKQIANPSTPSETKKPRSV----- 143  
  
 Qy           118 RIKQAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPF AHLTINATDIPS 177



```

                                     |||| |
Db      144 -----AHLTGNPR----- 151
Qy      178 GSHKVSLSWYHDRGWAKISNMTFNKGKLVNQDGFYYLYANICFRHHETSGDLATEYLQ 237
        | : | | | | | : : | | : | | : | : | : | : | : | : | : |
Db      152 -SRSIPL-EWEDTYGTALISGVKYKKGGLVINEAGLYFVYSKVYFRGQSCN----SQPLS 205
Qy      238 LMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESIEVSNPS 297
        ||: : | | ||: | : : : | : | | : : : | |
Db      206 HKVYM--RNFKYPGDLVLMEEKKLNICT-TGQIAHSSYLGAVERNLTVDHLYVNISQLS 262
Qy      298 LLDPDQDATYFGAFKV 313
        |:: :: |:: |::
Db      263 LINFEESKTFFGLYKL 278

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# RESULT 13

## TNF5\_CALJA

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ID      TNF5_CALJA      STANDARD;      PRT;      261 AA.
AC      Q9BDN3;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-
DE      L) (CD154 protein).
GN      TNFSF5 OR CD40LG OR CD40L.
OS      Callithrix jacchus (Common marmoset).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
OC      Callithrix.
OX      NCBI_TaxID=9483;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Lymphocytes;
RX      MEDLINE=21383618; PubMed=11491535;
RA      Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA      Weiss W.R., Ansari A.A.;
RT      "Cloning, sequencing, and homology analysis of nonhuman primate
RT      Fas/Fas-ligand and co-stimulatory molecules.";
RL      Immunogenetics 53:315-328(2001).
CC      -!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell
CC      proliferation in the absence of co-stimulus as well as IgE
CC      production in the presence of IL-4. Involved in immunoglobulin
CC      class switching (By similarity).
CC      -!- SUBUNIT: Homotrimer (By similarity).
CC      -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC      extracellular soluble form (By similarity).
CC      -!- PTM: The soluble form derives from the membrane form by
CC      proteolytic processing (By similarity).
CC      -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC      -----
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Query Match 10.1%; Score 169.5; DB 1; Length 261;  
Best Local Similarity 24.6%; Pred. No. 2.5e-07;  
Matches 71; Conservative 55; Mismatches 120; Indels 43; Gaps 15;

Qy	33	PPPPAPHPQPPAASRSMFVALLGLGL-GQVVCSVALFFYFRAQMDPNRISEDGTHCIYRIL	91
Db	8	PVPSAATGPPVSMKIFMYLLTVFLITQMIGSALFAVYLHRRLD--KIEDE-----R	57
Qy	92	RLHENADFQDT--TLESQDTKLIPDSCRRIKQAFQGAQVQKELQHIVGSQHIRAEKAMVDG	149
Db	58	NLHEDFVFMKTIQRCNTGERSLSLLNCEEIKSQFEGFV-KDIM-----LNKEEKKKEN	109
Qy	150	SWLDLAKRSKLEAQPFahlTINATDIPSGSHKVSLSswYHdRGWAKISN--MTFSNGK-L	206
Db	110	SF-EMQKGdQ-NPQIAAHVISEAS-----SKTTSVLQW-AEKGYTMSNNLVTLENGKQL	161
Qy	207	IVNQDGFYYLYANICFRHHETSGDLATEYLQLMVVYTKTSIKIPS--SHTLMKGGSTKYW	264
Db	162	TVKRQGLYYIYAQVTFCSNREASSQAP-----FIASLCLKPPNRFERILLRAANTH--	212
Qy	265	SGNSEFHfYSINVGgFFKLRSgEEISIEVSNPSLLDPDQATYfGAfKV	313

## RESULT 14

## TNF5\_AOTTR

ID TNF5\_AOTTR STANDARD; PRT; 261 AA.  
AC Q9BDM3;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-L) (CD154 protein).  
GN TNFSF5 OR CD40LG OR CD40L.  
OS Aotus trivirgatus (Night monkey) (Douroucoulis).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.  
OX NCBI\_TaxID=9505;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymphocytes;  
RX MEDLINE=21383618; PubMed=11491535;  
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P., Weiss W.R., Ansari A.A.;  
RT "Cloning, sequencing, and homology analysis of nonhuman primate Fas/Fas-ligand and co-stimulatory molecules.";  
RT Immunogenetics 53:315-328(2001).  
CC -!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell proliferation in the absence of co-stimulus as well as IgE production in the presence of IL-4. Involved in immunoglobulin class switching (By similarity).  
CC -!- SUBUNIT: Homotrimer (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).  
CC -!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).  
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.  
CC -----  
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CC -----  
DR EMBL; AF344860; AAK37542.1; -.  
DR HSSP; P29965; 1ALY.  
DR GO; GO:0016021; C:integral to membrane; ISS.  
DR GO; GO:0005174; F:CD40 receptor binding; ISS.  
DR GO; GO:0042100; P:B-cell proliferation; ISS.  
DR GO; GO:0006954; P:inflammatory response; ISS.  
DR GO; GO:0007159; P:leukocyte cell adhesion; ISS.  
DR GO; GO:0030168; P:platelet activation; ISS.  
DR InterPro; IPR003263; TNF\_5.  
DR InterPro; IPR006052; TNF\_family.  
DR InterPro; IPR008983; TNF\_like.  
DR InterPro; IPR003636; TNF\_subf.

DR	Pfam; PF00229; TNF; 1.			
DR	PRINTS; PR01702; CD40LIGAND.			
DR	ProDom; PD008600; TNF_5; 1.			
DR	ProDom; PD002012; TNF_subf; 1.			
DR	SMART; SM00207; TNF; 1.			
DR	PROSITE; PS00251; TNF_1; 1.			
DR	PROSITE; PS50049; TNF_2; 1.			
KW	Cytokine; Transmembrane; Glycoprotein; Signal-anchor.			
FT	CHAIN	1	261	TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT				MEMBER 5, MEMBRANE FORM.
FT	CHAIN	113	261	TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT				MEMBER 5, SOLUBLE FORM (BY SIMILARITY).
FT	DOMAIN	1	22	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	23	43	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT				(POTENTIAL).
FT	DOMAIN	44	261	EXTRACELLULAR (POTENTIAL).
FT	SITE	112	113	CLEAVAGE (BY SIMILARITY).
FT	DISULFID	178	218	POTENTIAL.
FT	CARBOHYD	240	240	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	261 AA;	29357 MW;	85E1588B507901B5 CRC64;

Qy	31	HAPPPPAHPQPPAASRSMFVALLGLGL-GQVVCVSAFFFYFRAQMDPNRISEDGTHCIYR	89
		:   :     :     :     :   :   :   :	
Db	6	HQPAPRSAATGLPVSMKIFMYLLTVFLITQMIGSALFAVYLHRRLD--KIEDE-----	56
Qy	90	ILRLHENADFQDT--TLESQDTKLIPDSCRRIKQAFQGAQVQKELQHIVGSQHIRAEKAMV	147
		:     : :   :       :     :   :   :	
Db	57	-RNLHEDFVFMKTIQRCNTGERSLSLLNCEEIKSQFEGFV-KDIM-----LNKEEKKK	107
Qy	148	DGSWLDLAKRSKLEAQPFahlTINATDIPSGSHKVSLSswYHdRGWAKISN--MTFSNGK	205
		:   : :   :     :   :   :   :   :   :   :	
Db	108	ENSF-EMQKGDQ-NPQIAAHVISEAS-----SKTTSVLQW-AEKGYTMSNNLVTLENGK	159
Qy	206	-LIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPS--SHTLMKGGSTK	262
		:     :     :   : :   : :   :   :   :	
Db	160	QLTVKRQGLYYIYAQVTFCSNREASSQAP-----FIASLCLKPPNRFERILLRAANTH	212
Qy	263	YWSGNSEFHfYSINVGgFFKLRSgEEISIEVSNPSLLDPDQATYfGAFKV	313
		:     :     :   : :   : :   :   :   :	
Db	213	--SSAKPCGQOOSIHLGGIFELQPGASVFVNVTDPsoVSHGTGFTSFGLLKL	261

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93076854; PubMed=1280226;  
 RA Graf D., Korthaeuer U., Mages H.W., Senger G., KroczeK R.A.;  
 RT "Cloning of TRAP, a ligand for CD40 on human T cells.";  
 RL Eur. J. Immunol. 22:3191-3194(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93049181; PubMed=1385114;  
 RA Hollenbaugh D., Grosmaire L.S., Kullas C.D., Chalupny J.N.,  
 RA Braesch-Andersen S., Noelle R.J., Stamenkovic I., Ledbetter J.A.,  
 RA Aruffo A.;  
 RT "The human T cell antigen gp39, a member of the TNF gene family, is a  
 RT ligand for the CD40 receptor: expression of a soluble form of gp39  
 RT with B cell co-stimulatory activity.";  
 RL EMBO J. 11:4313-4321(1992).  
 RN [3]  
 RP SEQUENCE FROM N.A., AND VARIANTS HIGM1 128-ARG-GLY-129 AND PRO-235.  
 RX MEDLINE=93145330; PubMed=7678782;  
 RA Aruffo A., Farrington M., Hollenbaugh D., Li X., Milatovich A.,  
 RA Nonoyama S., Bajorath J., Grosmaire L.S., Stenkamp R., Neubauer M.,  
 RA Roberts R.L., Noelle R.J., Ledbetter J.A., Francke U., Ochs H.D.;  
 RT "The CD40 ligand, gp39, is defective in activated T cells from  
 RT patients with X-linked hyper-IgM syndrome.";  
 RL Cell 72:291-300(1993).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93094757; PubMed=1281209;  
 RA Spriggs M.K., Armitage R.J., Strockbine L., Clifford K.N.,  
 RA Macduff B.M., Sato T.A., Maliszewski C.R., Fanslow W.C.;  
 RT "Recombinant human CD40 ligand stimulates B cell proliferation and  
 RT immunoglobulin E secretion.";  
 RL J. Exp. Med. 176:1543-1550(1992).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93138085; PubMed=7678552;  
 RA Gauchat J.F.M., Aubry J.-P., Mazzei G.J., Life P., Jomotte T.,  
 RA Elson G., Bonnefoy J.Y.;  
 RT "Human CD40-ligand: molecular cloning, cellular distribution and  
 RT regulation of expression by factors controlling IgE production.";  
 RL FEBS Lett. 315:259-266(1993).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA Shimadzu M., Terasaki H., Ninomiya R., Shimizu S., Nunoi H.,  
 RA Matsuda I.;  
 RL Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.  
 RN [7]  
 RP SEQUENCE OF 113-117, AND PROCESSING.  
 RX MEDLINE=96198042; PubMed=8626375;  
 RA Pietravalle F., Lecoanet-Henchoz S., Blasey H., Aubry J.-P., Elson G.,  
 RA Edgerton M.D., Bonnefoy J.-Y., Gauchat J.-F.;  
 RT "Human native soluble CD40L is a biologically active trimer, processed  
 RT inside microsomes.";

RL J. Biol. Chem. 271:5965-5967(1996).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 116-261.  
 RX MEDLINE=96131874; PubMed=8589998;  
 RA Karpsusas M., Hsu Y.-M., Wang J.-H., Thompson J., Lederman S.,  
 RA Chess L., Thomas D.;  
 RT "2-A crystal structure of an extracellular fragment of human CD40  
 RT ligand.";  
 RL Structure 3:1031-1039(1995).  
 RN [9]  
 RP 3D-STRUCTURE MODELING OF COMPLEX WITH CD40.  
 RX MEDLINE=98266353; PubMed=9605317;  
 RA Singh J., Garber E., van Vlijmen H., Karpsusas M., Hsu Y.-M.,  
 RA Zheng Z., Naismith J.H., Thomas D.;  
 RT "The role of polar interactions in the molecular recognition of CD40L  
 RT with its receptor CD40.";  
 RL Protein Sci. 7:1124-1135(1998).  
 RN [10]  
 RP VARIANTS HIGM1 ARG-36 AND GLY-140.  
 RX MEDLINE=93156839; PubMed=7679206;  
 RA Korthaeuer U., Graf D., Mages H.W., Briere F., Padayachee M.,  
 RA Malcolm S., Ugazio A.G., Notarangelo L.D., Levinsky R.J.,  
 RA Kroczeck R.A.;  
 RT "Defective expression of T-cell CD40 ligand causes X-linked  
 RT immunodeficiency with hyper-IgM.";  
 RL Nature 361:539-541(1993).  
 RN [11]  
 RP VARIANT HIGM1 GLU-123.  
 RX MEDLINE=93156840; PubMed=8094231;  
 RA Disanto J.P., Bonnefoy J.Y., Gauchat J.F.M., Fischer A.,  
 RA de Saint Basile G.;  
 RT "CD40 ligand mutations in X-linked immunodeficiency with hyper-IgM.";  
 RL Nature 361:541-543(1993).  
 RN [12]  
 RP VARIANTS HIGM1 PRO-155; ASP-211 AND VAL-227.  
 RX MEDLINE=93174270; PubMed=7679801;  
 RA Allen R.C., Armitage R.J., Conley M.E., Rosenblatt H., Jenkins N.A.,  
 RA Copeland N.G., Bedell M.A., Edelhoff S., Distech C.M.,  
 RA Simoneaux D.K., Fanslow W.C., Belmont J.W., Spriggs M.K.;  
 RT "CD40 ligand gene defects responsible for X-linked hyper-IgM  
 RT syndrome.";  
 RL Science 259:990-993(1993).  
 RN [13]  
 RP VARIANTS HIGM1 ALA-126; ARG-140 AND GLU-144.  
 RX MEDLINE=95233438; PubMed=7717401;  
 RA Macchi P., Villa A., Strina D., Sacco M.G., Morali F., Brugnoli D.,  
 RA Giliani S., Mantuano E., Fasth A., Andersson B., Zegers B.J.M.,  
 RA Cavagni G., Reznick I., Levy J., Zan-Bar I., Porat Y., Airo P.,  
 RA Plebani A., Vezzoni P., Notarangelo L.D.;  
 RT "Characterization of nine novel mutations in the CD40 ligand gene in  
 RT patients with X-linked hyper IgM syndrome of various ancestry.";  
 RL Am. J. Hum. Genet. 56:898-906(1995).  
 RN [14]  
 RP VARIANTS HIGM1 PRO-155 AND VAL-227, AND VARIANT ARG-219.  
 RX MEDLINE=96133533; PubMed=8550833;  
 RA Lin Q., Rohrer J., Allen R.C., Larche M., Greene J.M., Shigeoka A.O.,  
 RA Gatti R.A., Derauf D.C., Belmont J.W., Conley M.E.;

RT "A single strand conformation polymorphism study of CD40 ligand.  
RT Efficient mutation analysis and carrier detection for X-linked hyper  
RT IgM syndrome.";  
RL J. Clin. Invest. 97:196-201(1996).  
RN [15]  
RP VARIANTS HIGM1 ARG-36; CYS-140; SER-231; MET-254 AND GLY-227 DEL.  
RX MEDLINE=97295077; PubMed=9150729;  
RA Nonoyama S., Shimadzu M., Toru H., Seyama K., Nunoi H., Neubauer M.,  
RA Yata J.-I., Och H.D.;  
RT "Mutations of the CD40 ligand gene in 13 Japanese patients with  
RT X-linked hyper-IgM syndrome.";  
RL Hum. Genet. 99:624-627(1997).  
CC -!- FUNCTION: Mediates B-cell proliferation in the absence of co-  
CC stimulus as well as IgE production in the presence of IL-4.  
CC Involved in immunoglobulin class switching.  
CC -!- SUBUNIT: Homotrimer.  
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an  
CC extracellular soluble form.  
CC -!- TISSUE SPECIFICITY: Specifically expressed on activated CD4+  
CC T-lymphocytes.  
CC -!- PTM: The soluble form derives from the membrane form by  
CC proteolytic processing.  
CC -!- DISEASE: Defects in TNFSF5 are the cause of X-linked  
CC immunodeficiency with hyper-IgM type 1 (HIGM1) [MIM:308230]. HIGM1  
CC is an immunoglobulin isotype switch defect characterized by  
CC elevated concentrations of serum IgM and decreased amounts of all  
CC other isotypes. Affected males present at an early age (usually  
CC within the first year of life) recurrent bacterial and  
CC opportunistic infections, including pneumocystis carinii pneumonia  
CC and intractable diarrhea due to cryptosporidium infection. Despite  
CC substitution treatment with intravenous immunoglobulin, the  
CC overall prognosis is rather poor, with a death rate of about 10%  
CC before adolescence.  
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.  
CC -!- DATABASE: NAME=CD40Lbase;  
CC NOTE=European CD40L defect database (mutation db);  
CC WWW="http://www.expasy.org/cd40lbase/";  
CC FTP="ftp://ftp.expasy.org/databases/cd40lbase".  
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD154 entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd154.htm".

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CC -----

DR EMBL; X68550; CAA48554.1; -.  
DR EMBL; Z15017; CAA78737.1; -.  
DR EMBL; X67878; CAA48077.1; -.  
DR EMBL; L07414; AAA35662.1; -.  
DR EMBL; D31797; BAA06599.1; -.  
DR EMBL; D31793; BAA06599.1; JOINED.  
DR EMBL; D31794; BAA06599.1; JOINED.  
DR EMBL; D31795; BAA06599.1; JOINED.

DR EMBL; D31796; BAA06599.1; JOINED.  
 DR PIR; S28017; I53476.  
 DR PDB; 1ALY; 17-SEP-97.  
 DR PDB; 1I9R; 22-MAY-02.  
 DR Genew; HGNC:11935; TNFSF5.  
 DR MIM; 300386; -.  
 DR MIM; 308230; -.  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0005625; C:soluble fraction; TAS.  
 DR GO; GO:0005174; F:CD40 receptor binding; IPI.  
 DR GO; GO:0006916; P:anti-apoptosis; IDA.  
 DR GO; GO:0042100; P:B-cell proliferation; IDA.  
 DR GO; GO:0006954; P:inflammatory response; IDA.  
 DR GO; GO:0045190; P:isotype switching; ISS.  
 DR GO; GO:0007159; P:leukocyte cell adhesion; NAS.  
 DR GO; GO:0030168; P:platelet activation; IDA.  
 DR GO; GO:0007165; P:signal transduction; ISS.  
 DR InterPro; IPR003263; TNF\_5.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.

Query Match 9.4%; Score 158.5; DB 1; Length 261;  
 Best Local Similarity 24.5%; Pred. No. 2.3e-06;  
 Matches 68; Conservative 53; Mismatches 113; Indels 43; Gaps 15;

Qy	45	SRSMFVALLGLGL-GQVVC	SVALFFYFRAQMDPNRI	SEDGTHCIYRILRLHEN	ADFQDT-	102
		: :    :    ::	: :   :  ::	:		
Db	20	SMKIFMYLLTVFLITQ	MIGSALFAVYLHRR	LD--KIEDE-----	RNLHEDFVFMKTI	69
Qy	103	-TLESQDTKLIPDSCR	RRIKQAFQGAVQKEL	QHIVGSQHIRAEKAM	VDGSWLDLAKRSKLE	161
		: :   :       :    :	: :   :   :  :	:   :   :  :	:   :	
Db	70	QRCNTGERSLSLLN	C EEIKSQFEGFV-	KDIM-----	LNKEETKKENSEF-	EMQKGDQ-N 119
Qy	162	AQPFAHLTINATDIP	SGSHKVSLSWYH	DRGWAKISN--	MTFSNGK-LIVNQD	GFYYLYA 218
		:   :   :	:  :  :	:         :	:    :	
Db	120	PQIAAHVISEAS----	SKTTSVLQW-AE	KGYTMSNNLV	TLENGKQLTVKRQ	GLYYIYA 173
Qy	219	NICFRHHETSGDL	ATEYLQLMVYV	TKTSIKIPS--	SHTLMKGGSTKY	WSGNSEFHFYSIN 276
		:   : :   : :	:    :  :	:  :    :	:	
Db	174	QVTFCSNREASSQAP-----	FIASLCLKSPGR	FERILLRAANTH--	SSAKPCGQQSIH	224
Qy	277	VGGFFKLRS	GEEISIEVSNPS	LLDPDQDATY	FGAFKV	313
		:    : :   : :	:    :	:		
Db	225	LGGVFELQPGASV	FVNVTDP	SQVSHGTG	FTSFGLLKL	261

Search completed: September 15, 2004, 08:32:55  
 Job time : 25 secs